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November 15, 2004, 18:39:31; Search time 158 Seconds (without alignments) 862.767 Million cell updates/sec
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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Result		Query				
	Score	Match	Match Length DB	DB	ID	Description
	2085	100.0	380		AAB6	Aab66988 Mur
	2085	100.0	380		ADM28827	Adm28827 Human o
m	2085	100.0	381	æ	ADM28870	Adm28870 Human (
4	2085	100.0	382		ADM28869	Adm28869 Human (
2	2085	100.0	385		ADM28876	Adm28876 Human (
9	2085	100.0	391	ω	ADM28877	Adm28877 Human (
7	2085	100.0	400		ABU08820	Abu08820 Human
8	2085	100.0	401		AAW38345	
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12	2085	100.0	401		ABP55109	
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15	2085	100.0			ADM28813	Adm28813 Human
16	2085	100.0	537	ø	AA019639	Aao19639 Human
17	2080	99.8			ABG73895	Abg73895 Human (
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21	2079	99.7	00		ADF15245	Adf15245 Human
22	2079	99.7	380		ADM28860	Adm28860 Human
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ALIGNMENTS

RESULT 1

Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia; multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation; systemic lupus erythematosus; graft-versus-host disease; septic shock; acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain; coronary condition; myocardial infarction; cancer; diabetes; psoriasis; endometriosis; fever; glomerulonephritis; inflammatory bowel disease; AAB66988 standard; protein; 380 AA Murine OPG cysteine-rich domain. ischaemia; Parkinson's disease (first entry) 19-APR-2001 AAB66988; AAB66988

WO200103719-A2. Mus sp.

18-JAN-2001.

37-JUL-2000; 2000WO-US018667. 99US-00350670. 09-JUL-1999; 09-DEC-1999;

(AMGE-) AMGEN INC.

Chang M, Senaldi G; Calzone FJ, Lacey DL, Boyle WJ,

WPI; 2001-103031/11.

Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor necrosis factor alpha.

Disclosure; Fig 12; 316pp; English.

The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66976. in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet

Chang

Calzone FJ,

Lacey DL,

Boyle WJ,

WPI; 2004-041572/04.

BOYLE W J. LACEY D L. CALZONE F J. CHANG M.

(BOYL/) (LACE/) (CALZ/) (CHAN/)

96US-00706945. 96US-0077177. 98US-00132985. 95US-00577788

22-DEC-1995; 03-SEP-1996; 20-DEC-1996; 12-AUG-1998;

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conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematioss (SLB) and graft-versus-host disease (GvHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosalerosis, coronary conditions (e.g. wyocardial infanction), cancer, diabetes, endometriosis, fever, glomerulomephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock
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100.0%; Pred. No. 5.2e-153;
ive 0; Mismatches 0;
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Paget's disease of bone; hypercalcaemia; hyperparathyroidism; steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis; osteolytic metastasis; periodontal bone loss; Cushing's syndrome; acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome; Riley-day syndrome; immobilisation of extremity; tumnour; haematcologic malignancy; multiple mealome; haphoma; leukaemia; renal function disorder; osteopaenia; osteonecrosis; bone cell death;
                                                                                                                   Human osteoprotegerin cysteine-rich domains 1-4 plus C-terminus #1
                                                                                                                                                       OPG; bone resorption; excessive bone loss; osteoporosis;
                ADM28827 standard; protein; 380 AA
                                                                                                                                                                                                                                                                                             transgenic
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                           osteoprotegerin;
                                                                                   20-MAY-2004
ADM2882
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YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL ; 0 100.0%; Score 2085; DB 8; Length 380; 100.0%; Pred. No. 5.2e-153; Mismatches 100.08; FI Conservative Similarity Local Similes 380; 61 Query Match Best Loca Matches ò 엄 ò

99US-00405032

24-SEP-1999;

US2003207827-A1.

Mus sp.

Tegions (and an activity of increasing bone density), an antibody (Ab) or regions (and an activity of increasing bone density), an antibody (Ab) or its fragment which specifically binds to OPG, a composition comprising OPG (in a carrier, adjuvant, solubiliser and/or anti-oxidant) and an osteoprotegerin multimer consisting of osteoprotegerin monomers. Ab is useful for detecting the presence of OPG in a biological sample which Ab under conditions that allow binding of ab to OPG and detecting the bound Ab. OPG is useful for washing the levels of OPG in an animal (human). The nucleic assessing the ability of a candidate substance to bind to OPG. OPG NA is useful for regulating the levels of OPG in an animal (human). The nucleic acid promotes an increasing in tissue level of OPG. OPG is useful for treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced osteopaenia, bone loss due to rheumatoid arthritis, bone loss use to osteopychic metastasis, and periodontal bone loss. The method further involves administering a substance chosen from bone concepted further involves administering a substance chosen from bone concepted in thibitor, TWFalpha inhibitors, parathyroid hormone and their analogues, concepted in the protein and their analogues, protein and their analogues, protein and protein and excepted in a corresponsis, end once enhancing minerals. OPG is useful for treating osteoporosis such as primary osteoporosis, endocrine of excepted and processis and acromedally in the concepted in the analogue of the concepted in the concepted i The invention relates to a purified and isolated polypeptide having osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or having amino terminus at residue 22, and 1-216 amino acids are deleted from carboxy terminus of human OPG polypeptide. Also included are an isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression vector comprising OPG NA, a host cell transformed or transfected with the vector, a transgenic mammal comprising the cell, producing OPG, a polypeptide comprising an amino acid sequence of at least about 164 amino acids comprising four cysteine-rich domains characteristic of the cysteine rich domains characteristic or the cysteine rich domains characteristic or cysteine rich domains characteristic or cysteine rich domains characteristic or cysteine rich do hereditary and congenital forms of osteoporosis (osteogenesis imperfecta homocystinuria, Menke's syndrome, and Riley-day syndrome) and osteoporosis due to immobilisation of extremities, hypercalcaemia resulting from solid tumours and haematologic malignancies (multiple Novel osteoprotegerin useful for treating conditions resulting in bone loss such as osteoporosis, hypercalcemia, Paget's disease of bone, bone loss caused by rheumatoid arthritis or osteomyelitis. or bone cell hypercalcaemia associated with hyperthyroidism and renal function lymphoma and leukaemia), idiopathic hypercalcaemia, and present sequences is an OPG protein (or fragment) disorders, osteopaenia following surgery and osteonecrosis death. The present sequences is an OPG protein (or fragment Disclosure; SEQ ID NO 139; 141pp; English. Sequence 380 AA; myeloma,

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                                     1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
Gaps
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us-10-676-358-1.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                     excessive bone loss; osteoporosis;
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CALZONE F J.
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myeloma, Iymphoma and leukaemia), idiopathic hypercalcaemia, and hypercalcaemia associated with hyperthyroidism and renal function disorders, osteopaenia following surgery and osteonecrosis or bone death. The present sequences is an OPG truncation/deletion or

substitution mutant protein (or fragment).

costeoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or having amino terminus at residue 22 and 1-216 amino acids are deleted from catboxy terminus of human OPG polypeptide. Also included are an isolated nucleic acid encoding an OPG polypeptide (OPG NR), an expression comprising oPG NA, a host cell transformed or transfected with the vector comprising oPG NA, a host cell transformed or transfected with the vector comprising oPG NA, a host cell transformed or transfected with the oplypeptide comprising an amino acid sequence of at least about 164 amino cypreptide comprising an amino acid sequence of at least about 164 amino cysteine rich domains of tumour necrosis factor receptor extracellular cysteine rich domains of tumour necrosis factor receptor extracellular cysteine rich domains of tumour necrosis factor receptor extracellular cysteine rich domains of tumour necrosis factor receptor extracellular cype in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) ope (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) ope (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) ope (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) ope (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) ope (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant) of stabiliser and/or anti-oxidant and accordant and detecting the bound Ab. Opg is useful for catecting the sample with Ab under conditions that allow assessing the ability of a candidate substance to bind to Opg. Opg is useful for requiring the levels of Opg in a pind to Opg. Opg is useful for requiring the levels of Opg in an animal (human). The nucleic acid promotes an increasing in excessive bone loss, osteoporosis, Pager's cateoparally bone loss due to rheumatoid arthritis, bone loss due to creating a bone deceptored promotes and because and parter and page of osteoporosis (hyperthyroidism, Cushing's syndrome, and second congenia in morbilisation of extremi

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OKLFLEMIGNQVQSVKISCL 380 362 OKLFLEMÍGNOVOSVKÍSCL 381

361

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Novel osteoprotegerin useful for treating conditions resulting in bone loss such as osteoporosis, hypercalcemia, Paget's disease of bone, bone loss caused by rheumatoid arthritis or osteomyelitis.

Chang M;

Calzone FJ,

Boyle WJ, Lacey DL, WPI; 2004-041572/04.

CHANG M.

(CALZ/)

The invention relates to a purified and isolated polypeptide having

Claim 37; Page; 141pp; English.

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Novel osteoprotegerin useful for treating conditions resulting in bone loss such as osteoporosis, hypercalcemia, Paget's disease of bone, bone loss caused by rheumatoid arthritis or osteomyelitis.
                                                                                            Human, OPG; bone resorption; excessive bone loss; osteoporosis; Paget's disease of bone; hypercalcaemia; hyperparathyroidism; steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis; osteolytic metastasis; periodontal bone loss; Cushing's syndrome; Riley-day syndrome; immobilisation of extremity; tumour; haematologic malignancy; multiple myeloma; lymphoma; leukaemia; haematologic malignancy; multiple myeloma; lymphoma; leukaemia; renal function disorder; osteopaenia; osteonecrosis; bone cell death; osteoprotegerin; transgenic; mutant; mutein.
                                                                          Human OPG truncation mutant, OPG met-lys[22-401].
                                                                                                                                                                                                                                                                                                                                                                                                                   Chang M;
          ADM28869 standard; protein; 382 AA.
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96US-00706945.
96US-00771777.
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                                                     (first entry)
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LACEY D L.
CALZONE F J.
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(CALZ/) CALZONE F
(CHAN/) CHANG M.
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03-SEP-1996;
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                                                     20-MAY-2004
                                                                                                                                                                                                                                                                                                                            20-DEC-1996;
                                                                                                                                                                                                                                                              06-NOV-2003
                                                                                                                                                                                                                    Synthetic
                               ADM28869:
ADM28869
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costeoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or having amino terminus at residue 22, and 1-216 amino acids are deleted from carboxy terminus at residue 22, and 1-216 amino acids are deleted from carboxy terminus at human ope polypeptide. Also included are an isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression vector, a transgenic mammal comprising the cell, producing OPG, a comprising operation of a least about 164 amino acids comprising the cell, producing OPG, a compressing four cysteine-rich domains characteristic of the acids comprising an amino acid sequence of at least about 164 amino acids comprising four cysteine-rich domains characteristic of the acids comprising four cysteine-rich domains characteristic of the acids comprising four cysteine-rich domains characteristic of the acids comprising four specifically binds to OPG, a composition comprising its fragment which specifically binds to OPG, a composition comprising companies and an osteoprotegerin multimer consisting of osteoprotegerin monomers. Ab is useful for detecting the presence of OPG in a biological sample which involves incubating the sample with Ab under conditions that allow binding of ab to OPG and detecting the bound Ab. OPG is useful for assessing the ability of a candidate substance to bind to OPG OPG NA is useful for regulating the levels of OPG oPG in an animal (human). The nucleic acid promotes an increasing in tissue level of OPG. OPG is useful for treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced The invention relates to a purified and isolated polypeptide having Claim 37; Page; 141pp; English

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osteonyelitis, osteolytic metastasis, and periodontal bone loss. The method further involves administering a substance chosen from bone method further involves administering a substance chosen from bone method fortein BMP-1 through BMP-12, TGF-beta family members, IL-1 inhibitor, TMFalpha inhibitors, parathyroid hormone and their analogues, parathyroid hormone related protein and their analogues, E series of prostaglandins, bisphosphonates, and bone-enhancing minerals. ORG is useful for treating osteoporosis such as primary osteoporosis, endocrine osteoporosis (hyperthyroidism, Cushing's Syndrome, and acromegaly), hereditary and congenital forms of osteoporosis (osteogenesis imperfecta horditary and congenital forms of osteoporosis (usufing) and softenessis in the cesulting from solid tumours and haematologic malignancies (multiple myencalcaemia associated with hyperthyroidism and renal function disorders, osteopaenia following surgery and osteonecrosis or bone cell chemistric the present sequences is an OPG truncation/deletion or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLBIEFCLKHRSCPPGFGVVQAGTPERNTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 2085; DB 8; Length 382; Best Local Similarity 100.0%; Pred. No. 5.2e-153; Matches 380; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders, osteopaenia following surgery and osteomecrosis or bone cell death. The present sequences is an OPG truncation/deletion or substitution mutant protein (or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel osteoprotegerin useful for treating conditions resulting in bone loss such as osteoporosis, hypercalcemia, Paget's disease of bone, bone loss caused by rheumatoid arthritis or osteomyelitis.
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96US-00706945.
96US-00771777.
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LACEY D L.
CALZONE F J.
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Homo sapiens.
Synthetic.
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20-DEC-1996;
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(LACE/)
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0 180 240 125 185 245 306 SDQILKLLSLWRIKNGDQDTLKGLMALKASKTYHFPKTVTQSLKKTIRFLHSFTWYKLY 365 120 9 65 Paget's disease of bone, hypercalcaemia; hyperparathyroidism; steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis; osteolytic metastasis; periodontal bone loss; Cushing's syndrome; acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome; Riley-day syndrome; immobilisation of extremity; tumour; haematologic malignancy; multiple myeloma; lymphoma; leukaemia; renal function disorder; osteopaenia; osteonecrosis; bone cell death; 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 126 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN 186 CEEAFFREAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN 246 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 66 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIBFCLKHRSCPPGFGVVQAGTPERNTV 241 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQIRSLMESLPGKKVGAEDIEKTIKACKP ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 301 SDQILKLISLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY Gaps Human OPG truncation mutant, OPG met-met-arg-gly-ser-(His)6[22-401] OPG; bone resorption; excessive bone loss; osteoporosis; .. 0 Length 385; Indels 100.0%; Score 2085; DB 8; 100.0%; Pred. No. 5.2e-153; ive 0; Mismatches 0; osteoprotegerin; transgenic; mutant; mutein. Calzone FJ, Chang M; ADM28877 standard; protein; 391 AA. 366 OKLFLEMIGNOVOSVKISCL 385 OKLFLEMIGNOVQSVKISCL 380 100.0%; F1. 95US-00577788. 96US-00706945. 96US-0077177. 98US-00132985 99US-00405032 (first entry) 380; Conservative Lacey DL, BOYLE W J.
LACEY D L.
CALZONE F J
CHANG M. Query Match Best Local Similarity Matches 380; Conserv JS2003207827-A1 22-DEC-1995; 03-SEP-1996; 20-DEC-1996; 24-SEP-1999; 20-MAY-2004 12-AUG-1998 06-NOV-2003 Boyle WJ, Synthetic 361 ADM28877; 121 (BOYL/) CHAN/) LACE/) RESULT 6 ADM28877 THE STATE OF STATES OF STA

The invention relates to a purified and isolated polypeptide having osteoprotegerin (DEP), an OPG polypeptide from rat, human and mouse, or baving amino terminus at residue 22, and 1-216 amino acids are deleted to seteoprotegerin (DEP), an OPG polypeptide (DOF NA), an expression usolated muclaic acid encoding an OPG polypeptide (OPG NA), an expression coefficial caid encoding an OPG polypeptide (OPG NA), an expression coefficial and an opg polypeptide comprising of NA, a host cell transformed or transfected with the coefficial and annual comprising the cell, producing OPG, a composition of the comprising of the cell, producing OPG, a composition of the comprising of the cell, producing OPG, a composition of the comprising of the composition of the composition of the composition of the coefficially phing to OPG, a composition of comprising of the composition of the coefficially phing the Dependence of OPG, a composition of the coefficial operation of the coefficial of the presence of OPG, a composition of the coefficial operation of the coefficial operation of the presence of OPG, a composition of the coefficial operation of the presence of OPG, a composition of the coefficial operation of the presence of OPG, a composition of the coefficial operation of the presence of OPG, a composition of the coefficial operation of the presence of OPG, a composition of the coefficial operation of the presence of OPG in a biological sample with the levels of OPG in a biological sample with the presence of OPG in a biological sample of the coefficial operation of the levels of OPG in an animal (Numan). The nucleic acid promotes an increasing in tissue level of OPG, OPG is useful for cutal processing the levels of OPG in a periodorical post of coefficial operation of a coefficial operation of opera Novel osteoprotegerin useful for treating conditions resulting in bone loss such as osteoporosis, hypercalcemia, Paget's disease of bone, bone loss caused by rheumatoid arthritis or osteomyelitis. death. The present sequences is an OPG tra substitution mutant protein (or fragment) Claim 37; Page; 141pp; English WPI; 2004-041572/04.

Sequence 391 AA;

truncation/deletion or

Gaps · 0 DB 8; Length 391; 0; Indels 100.0%; Score 2085; DB 8; 100.0%; Pred. No. 5.3e-153; iive 0; Mismatches 0; Matches 380; Conservative Similarity 12 Query Match Local à d à

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9 71 ETPPPKYLHYDEETSHOLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL ETFPRXILHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL

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311 252 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 312 SDQILKLLSIWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY OKLFLEMIGNOVQSVKISCL 380 372 OKLFLEMIGNOVOSVKISCL 391 301 361 g g ð à

AA. ABU08820 standard; protein; 400 RESULT 7 ABU08820

ABU08820;

(first entry) 13-AUG-2003

Human osteoprotegerin protein.

Human; osteoprotegerin; endothelial morphogenesis; capillary formation. US2003022834-A1. Homo sapiens.

30-JAN-2003.

09-MAY-2002; 2002US-00142658.

10-MAY-2001; 2001US-0290230P.

(MALY) MALYANKAR U M. (SCAT/) SCATENA M. (GIAC/) GIACHELLI C M.

Giachelli CM; Scatena M, Malyankar UM,

WPI; 2003-479494/45. N-PSDB; ABX93089.

Promoting endothelial morphogenesis for promoting formation of blood vessels, e.g. capillaries, in vivo in an area of damaged mammalian heart muscle, involves providing osteoprotegerin to one or more endothelial

Claim 3; Page 9-10; 15pp; English.

morphogenesis, comprises providing osteoprotegerin to one or more endothelial calls. The invention also discloses an implantable medical device comprising a device body and a layer attached to a surface of the device body. The layer comprises a molecule such as osteoprotegerin or a nulmal body. The layer comprises a molecule such as osteoprotegerin or a capted to be completely or partially implanted into an animal body. The completely or partially implanted into an animal body. The method of the invention is useful for promoting in vivo endothelial comphogenesis, such as the formation of capillaries which are formed in formation of an endothelial lining in a blood vessel, an artificial or natural blood vessel. The method is also useful for promoting endothelial comphogenesis in vitro. The implanted medical device is useful for promoting endothelial morphogenesis in any situation, e.g. promotino of blood vessel growth in and around damaged heart muscle. The implanted medical device and foreign body reaction. The method is useful for promoting the formation of a collagenous capsule around the implanted medical device and foreign body reaction. The method is useful for promoting formation of blood vessels in vivo capsule around the implanted medical device and foreign body reaction. The method is useful for promoting formation of blood vessels in vivo capsule around the implanted medical device and foreign body reaction. The method is useful for promoting formation of blood vessels in vivo capsule around the implanted medical device and foreign body reaction. The method is useful for promoting formation of blood vessels in vivo capsule around the implanted medical device and foreign body reaction. The method of the invention to promote endothelial morphogenesis This invention relates to a novel method for promoting endothelial

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Osteoprotegerin; antibody; diagnosis; affinity purification; recombinant production; transgenic animal; treatment; prevention; antisense oligonucleotide; probe; detection; screening; human; bone disease; osteoporosis; Paget's disease; hypercalcaemia; hyperparathyroidism; rheumatoid arthritis; osteomyelitis; osteopatorytic metastasis; periodontal bone loss; bone necrosis; osteopaenia.
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                                                                                                                      61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                                 91 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIBPCLKHRSCPPGFGVVQAGTPBRNTV 140
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                                                                                                                                                                                                                                                                                                                       380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding osteoprotegerin - useful for treatment of diseases involving excessive bone loss, e.g. osteoporosis.
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                                                                                                                                                                                     141 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKGIDVTL
                                                                                                                                                                                                           CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN
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                                                                           1 ETFPPKYLHYDEETSHOLL.CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                                     Gaps
                                                     0;
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                               100.0%; Score 2085; DB 6;
100.0%; Pred. No. 5.5e-153;
iive 0; Mismatches 0;
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96US-00706945,
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                                          Best Local Similarity 100.
Matches 380; Conservative
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           Sequence 400
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03-SEP-1996;
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                                      The present sequence is human osteoprotegerin (OPG). Anti-OPG antibodies can be used in OPG diagnostic assays, and as affinity purification materials. The OPG cDNA can be used to express recombinant OPG and to generate transgenic animals. It can also be used to regulate the level of OPG in mammals, specifically to increase OPG levels, however the use of used as probes to detect OPG expressing cells and tissue, and to screen cDNA libraries for related sequences. OPG can be used to treat or prevent bene diseases, specifically excessive bone loss, e.g. osteoporosis, Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid arthritis, osteoporpulation metastases, periodontal bone loss,
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Claim 23; Page 109-111; 182pp; German.
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                                                                                                                                                                                                                                                                                                                                                                    bone necrosis and osteopaenia
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Matches 380; Conservative
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psoriasis; disease;

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The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated costeoproregerin (OPG) protein (ARFS1836-AAFS788 and ARB66974-AAB66976)

In conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibrobhast growth factor (FGF)1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLB) and graft-versus-host disease (GYHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's diseases, anorexia, cancer, diabetes, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                     Treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis and asthma, comprises administering an osteoprotegerin protein in conjunction with e.g. inhibitors of interleukin and tumor
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coronary condition, myocardial infarction; cancer; diabetes; endometriosis; fever; glomerulonephritis; inflammatory bowel
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100.0%; Pred. No. 5.5e-153;
ive 0; Mismatches 0;
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                      endometriosis; fever; glomerulc
ischaemia; Parkinson's disease.
                                                                                                                                                                                  07-JUL-2000; 2000WO-US018667.
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N-PSDB; AAF57838.
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                                                                           Homo sapiens
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09-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                   sequence represents the human osteoprotegrin (OPG). The invention
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                                                                                                                                                                                                                                                                                                             οĘ
                                                                                                                                                                                                                                                                                                                                                                  prevent cardiovascular diseases provides an alternative to invasive treatments. OPG can be used as a single therapeutic for prevention and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                   relates to a method of treating or preventing cardiovascular disease administering OPG. The method can be used to treat and prevent cardiovascular diseases associated with occlusion and calcification blood vessels, especially atherosclerosis or Monckeberg's arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat prevent cardiovascular diseases provides an alternative to invasive
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                                                                                                                                                                especially
                                                                                                                                                                                                                                                                                                                                                                                                  treatment of both osteoporosis and cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                 atherosclerosis and Monckeberg's arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 2085; DB 3;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0;
                                                                                                                                                            Treating and preventing cardiovascular diseases,
                                                                                                                                                                                                                    English.
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98US-00064832
                                                                                                                                                                                                                 9; Page 37-39; 43pp;
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                                                                     Sarosi I;
                                                                                                         2000-013182/01,
                                 (AMGE-) AMGEN INC.
                                                                                                                          N-PSDB; AAZ37254
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 401 AA;
23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel mutant proteins having an amino acid sequence that is different from and is at least about 70% identical to the amino acid sequence of human receptor activator of NRkappaB (hRANK) or human osteoprotegerin (hOPG), and which has a binding affinity to RANK ligand (RANKL) that is at least as high as the binding affinity of hRANK or hOPG to RANKL. as determined by functional competition assay. The protein of the invention may have osteopathic activity and may act as a RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity inhibitor. The nucleotide sequence shown in the invention may be used in gene therzapy. The protein of the invention or And in the preparation of a conficament for treating or preventing osteoporosis, or other bone confiscases or diseases associated with binding of RANKL to the RANK receptor. A host cell containing a vector expressing the protein is useful for producing a polypeptide having binding affinity to RANKL, where the polypeptide comprises at least one N- or O-glycosylation site and the host cell is a eukaryotic host cell capable of in vivo confugation, and/or the polypeptide is subjected to conjugation to a non-polypeptide molety in vitro. The protein of the invention has compressed functional in vivo half-life and/or serum half-life compared to the binding affinity of haRANK or hOPG and has an improved binding affinity to RANKL, as functional competition assay. The present sequence represents the human competition assay. The present sequence represents the human competition in protein used to generate the mutant
Novel human receptor activator of NFkappaB (hRANK) or human osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANKL; human receptor activator of NPkappaB; osteoprotegerin; OPG; RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Wild type human OPG (osteoprotegerin) protein.
                                                                                                                                                                                                                                                                       ABG71823 standard; protein; 401 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoporosis; bone disease; human.
                                                                                                                                      401
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                                                                                                                OKLFLEMIGNOVOSVKISCL
                                                                                    OKLFLEMIGNOVQSVKISCL
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23-MAR-2001; 2001US-0278320P.
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                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                          22 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
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                                                      Gaps
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  Length 401;
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100.0%; Score 2085; DB 5;
100.0%; Pred. No. 5.5e-153;
ive 0; Mismatches 0;
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                                                      Conservative
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                        Similarity
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Query Match
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The present sequence is the protein sequence of human osteoprotegerin (OPG) receptor. The invention provides methods of using OPG ligand (OPGL) of activate monocytes to secrete chemokines or cytokines by exposing a mammalian cell (in cell culture or in a mammal) to OPGL. Also provided are methods of using OPGL to treat conditions or diseases in mammals associated with, or resulting from lack of, or decreased, chemokine or cytokine secretion by monocytes. The invention also provides OPGL agonist and antagonist molecules to modulate immune activity. These may include and antagonist molecules to modulate immune activity. These may include condition, antibody, an anti-OPG or RAMK receptors. An antagonist comprising an anti-OPGL antibody, an anti-OPG receptor antibody, an anti-OPG receptor immunoadhesin or a RAMK receptor immunoadhesin is used in a claimed method of treating an immune-related condition, specially an autoimmune disease, rheumatoid arthritis, insulin dependent diabetes, osteoarthritis, inflammatory Dowel disease (especially
                       2B; 111pp; English
                       sclosure; Fig
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Sequence 401 AA;

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                                                                             1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                    Gaps
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100.0%; Score 2085; DB 6; Length 401; 100.0%; Pred. No. 5.5e-153; ive 0; Mismatches 0; Indels 0.
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                  Local Similarity 100.
1es 380; Conservative
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Human osteoprotegerin (OPG) protein. AAE34363 standard; protein; 401 AA (first entry) 14-MAY-2003 RESULT 13 AAE34363

Human, acute septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome, receptor activator of NF-kappa B; cancer; scu bone formation, rickets, Langerham's cell histicocytosis, gene the monoostotic fibrous dysplasia; radiation therapy, spinal cord inj. RANK, Gaucher's disease, polyostotic fibrous dysplasia; OPG; osteoprotegerin.

Homo sapiens

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The invention relates to a method of treating a patient having e.g. acute septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome or spinal cord injury. The method involves administering a receptor activator of NF-kappa B (RANK) antagonist to stimulate an increase in the rate for formation of new bone. RANK antagonist is capable of inhibiting the ability of RANK to induce NF-kappa B. The method is useful for stimulating bone formation, or for treating patients having acute septic arthritis, osteomalacia (including rickets and scurvy), hyperparathyroidism, Cushing's syndrome, monoostotic fibrous dysplasia, capinal cord injury, patients requiring periodontal reconstruction, or patients who have completed a course or radiation therapy for cancer. The method is also useful for treating a patient who is a prosthetic joint recipient, a bone graft recipient, or a ligament graft recipient. The invention is useful in gene therapy. The present sequence is human osteoprotegerin (OPG). OPG serves as human RANK
                                                                                                                                                                                                                                                                                                                                                                                                      Treating patients having e.g. acute septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome or spinal cord injury, comprises administering a receptor activator of NF-kappa B antagonist to increase
                                                                                     /note= "Mature OPG protein"
                                    1. .21
/label= Signal peptide
               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 47-49; S2pp; English
                                                                                                                                                                                                      17-MAY-2002; 2002WO-US016002
                                                                                                                                                                                                                                       17-MAY-2001; 2001US-0291919P
                                                                                                                                                                                                                                                                                                              Dougall WC, Anderson DM;
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                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP.
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N-PSDB; AAD52597.
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240 180 120 261 81 82 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIBFCLKHRSCPPGFGVVQAGTPERNTV CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 22 втерркулнурввтзнольсрксредтулконстакиктусарсррнуутраинтярвсь 61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGLDVTL 142 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGLDVTL 1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL Gaps 0; Indels 100.0%; Score 2085; DB 6; 100.0%; Pred. No. 5.5e-153; cive 0; Mismatches 0; 100.08; LL. Conservative Similarity Local Simi 241 121 181 202 Best Loca Matches

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scurvy; therapy;

Length 401;

Query Match

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Gaps

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Mismatches
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/note= "M
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380;
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ADM28813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a substance which is useful for the manufacture of a medicament for treating or preventing fibrotic disease.

The substance comprises: (a) a polypeptide comprising a fully defined sequence having 401 amino acids (see ADD01625 and ADD01627), or its amino acids 22-401 or 22-194; (b) a polypeptide comprising 1, 2, 3 or 4 acids 22-401 or 22-194; (b) a polypeptide comprising 1, 2, 3 or 4 acids 22-401 or 22-194; (b) a polypeptide comprising 1, 2, 3 or 4 acids 22-401 or 22-194; (b) a polypeptide comprising 1, 2, 3 or 4 acids 22-401 or 22-194; (b) and where any changes to the complement of the DNA sequence encoding (a)-(b) under moderately or highly stringent conditions are conservative amino acid sequence has at least 40, 50, 60, 70, 80 or 90% identity with (a)-(b); and where any changes in the amino acid sequence are conservative amino acid substitutions to the amino acid sequence are conservative, active fraction or circularly permutated derivative of (a)-(b); and wholypeptide comprising the 401-amino acid derivative, active fraction or circularly permutated derivative of (a)-(c). Also described: (1) a polypeptide comprising the 401-amino acid of costeoprotegerin; and (2) a method for tracting or preventing a fibrotic disease, particularly scleroderma. The substance has antiinflammatory costeoprotegerin; and (2) a method for tracting or polypeptide in a cell for the preparation of a medicament for treating or the nucleic acid molecule encoding a polypeptide of the invention can be conserved in a cell for the preparation of a medicament for treating or polypeptide in a cell for the preparation of a medicament for treating or greventing a fibrotic disease, in particular and sequence represents a human osteoprotegerin amino acid sequence which is sequence represents a human osteoprotegerin amino acid sequence which is
     SDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
                            322 SDQILKILSLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRPLHSFTWYKLY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a substance for the manufacture of a medicament for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fibrotic disease; cysteine-rich domain; osteoprotegerin; scleroderma; antiinflammatory; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human osteoprotegerin amino acid sequence SEQ ID NO:4.
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Pred. No. 5.5e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 4; 68pp; English.
                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                              382 QKLFLEMIGNQVQSVKISCL 401
                                                                                                                361 OKLFLEMIGNOVOSVKISCL 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing fibrotic disease.
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity
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                                                                                     82 YCSPVCKELQYVKQECNRTHNRVCECKEGRXLEIBFCLKHRSCPPGFGVVQAGTPERNIV
                                                                                                                                                                                                 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKROHSSQEOTFQLLKLWKHON
                                                                                                                                                                                                                         202 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN
                                                                                                                                                                                                                                                                                     262 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP
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                                                                                                                                                              142 CKRCPDGFFSNETSSKAPCRKHINCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVIL
                                                                                                                                                                                                                                                                     241 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSIMBSLPGKKVGAEDIEKTIKACKP
                             22 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                                              61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV
                                                                                                                                  CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL
ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Mature OPG, claimed in claim 24"
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/note= "Claimed in claim 35"
27. .185
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re= "Claimed in claim 32"
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:e= "Claimed in claim 35"
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/note= "Claimed in claim 32"
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The invention Felaces to a published and isolated polypeptic he having corresponded relates to a published and isolated polypeptic having anion cheminus at residue 22, and 1-216 amino acids are deleted having amino terminus of human OPC polypeptide (DPG NA), an expression isolated nucleic acid encoding an OPC polypeptide (OPC NA), an expression vector comprising OPC NA, a host cell transformed or transfected with the vector comprising OPC NA, a host cell transformed or transfected with the vector comprising OPC NA, a host cell transformed or transfected with the vector, a transgenic marmal comprising the cell, producing OPC, a polypeptide comprising of tumour necrosis factor receptor extracellular regions (and an activity of increasing bone density), an antibody (Ab) or its fragment which specifically binds to OPG, a composition comprising or ope fumour necrosis factor receptor antibody (Ab) or its fragment which specifically binds to OPG, a composition comprising and an activity of increasing bone desnity) and an inchedit of a carrier, adjuvant, solubliser, reabiliser and/or anti-oxidant) and an osteoproregarin multimer consisting of OSteoprotegarin monomers. OF its fragment which specifically binds to OPG, and on osteoproregarin multimer consisting of OSteoprotegarin multimer consisting of OPG in an animal (Muman). The nucleic which involves incubating the levels of OPG in an animal (Muman). The nucleic which involves incubating the levels of OPG in an animal (Muman). The nucleic setul for regulating the levels of OPG in an animal (Muman). The nucleic creating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced cite acting a bone disorder e.g. excessive bone loss due to renumaroid arthritis, osteolyric metastasis, and periodonral bone loss due to resulting from of the displantial for resulting from of correspondial to recent of osteoporosis, enclosed frame in opcomensation of extending a parathyroid hormone related provein and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoprotegerin useful for treating conditions resulting in bone such as osteoporosis, hypercalcemia, Paget's disease of bone, bone caused by rheumatoid arthritis or osteomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a purified and isolated polypeptide having
                32. .401
/note= "Claimed in claim 25"
/note= "Claimed in claim 35"
                                                                                                                                                                                                                                                                                                                                                                                     Chang M;
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96US-00771777.
98US-00132985.
                                                                                                                                                       99US-00405032
                                                                                                                                                                                           95US-00577788
                                                                                                                                                                                                                                                                                      (BOYL/) BOYLE W J.
(LACE/) LACEY D L.
(CALZ/) CALZONE F J.
(CHAN/) CHANG M.
                                                                                                                                                                                                                                                                                                                                                                                       Boyle WJ, Lacey DL,
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N-PSDB; ADM28812.
                                                                          US2003207827-A1
                                                                                                                                                                                                                                20-DEC-1996;
12-AUG-1998;
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Sequence 401 AA;

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                                                             ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                 Gaps
                               0;
 Length 401;
                               Indels
100.0%; Score 2085; DB 8;
100.0%; Pred. No. 5.5e-153;
ive 0; Mismatches 0;
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completed: November 15, 2004, 19:00:32 Job time : 164 secs Search

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Query Match
Best Local Similarity 100.
Matches 380; Conservative
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MOLECULE TYPE: protein

US-08-974-022-6
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-706-945D-128
US-08-577-788C-6
US-08-577-788C-56
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STATE: California
COUNTRY: USA
ZIP: 9120-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
US-08-706-945D-126

US-08-577-788C-4

US-08-577-788C-54

US-08-706-945D-141

US-08-8056A-18

US-08-577-788C-50

US-08-577-788C-50

US-09-532-277A-3

US-09-523-323-58

US-09-523-323-58

US-08-706-945D-136

US-08-706-945D-136
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                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BOYLE, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTBOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/974,022 FILING DATE: 12-DEC-1995 CLASSIFICATION: PEROR APPLICATION DATA: APPLICATION NUMBER: 08/577,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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amino acid
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ADDRESSEE: Amgen Inc
STREET: 1840 Dehavil
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100.0%; Score 2085; DB 3; Length 401; 100.0%; Pred. No. 2.4e-186; .ive 0; Mismatches 0; Indels 0;

61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIBFCLKHRSCPPGFGVVQAGTPERNTV 120

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121 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL
                                                                                                                                          142 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGLDVTL
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22 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
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APPLICATION NUMBER: US/08/795,445A
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100.0%; Pred. No. 2.4e-186;
tive 0; Mismatches 0;
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTROPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM is MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                      380
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Patent No. 6284485
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      YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPFGFGVVQAGTPERNTV 141
                                                                     CKRCPDGFFSNEISSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 180
                                                                                         142 CKRCPDGFFSNEISSKAPCRKHTNCSVFGLLIGKGNATHDNICSGNSESTQKCGIDVIL 201
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APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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SOFTWARE PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042,785A

FILING DATE: 17-MAR-1998

PRIOR APPLICATION NUMBER: US 08/938,896

FILING DATE: 26-52P-1997

ATTORNEY/AGENT INFORMATION:
NAME: MANDIAGEOUXES, AMY E

REGISTRATION NUMBER: 36,207

REFRENCE/POCKET NUMBER: 36,207

REFRENCE/COKET NUMBER: MEI-001CP

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 2.4e-186;
tive 0; Mismatches 0;
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28 State Street
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-042-785A-12
'Sequence 12, Application US/09042785A
'Patent No. 6194151
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 anino acids
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Best Local Similarity 100.0
Matches 380; Conservative
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internal
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COUNTRY: USA
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MEDIUM TYPE: Floppy
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FRAGMENT TYPE:
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CITY: Boston
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APPLICATION NUMBER: US/08/974,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BOYLE, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
ITILE OF INVENTION: OSTEOPROTECERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTONEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
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amino acid
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Best Local Similarity 100.0
Matches 380; Conservative
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                                                                                                                                                                                                                                                                                             241 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
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YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV
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; Pred. No. 2.4e-186;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,447A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
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Best Local Similarity 100.0%;
Matches 380; Conservative 0
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERRNEE/POCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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ZIP: 91362-1789
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Sequence 128, Application US/08706945D Patent No. 6369027 GENERAL INFORMATION:
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Best Local Similarity
Matches 380; Conserv
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                                                                                                     CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL
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MEDIUM TYPE: Rloppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 2085; DB 3;
100.0%; Pred. No. 2.4e-186;
live 0; Mismatches 0;
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APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTBOPROTEGERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08795446B
Patent No. 6288032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                 QKLFLEMIGNQVQSVKISCL 380
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REFERENCE/DOCKET UNMBER:
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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CITY: Thousand Oaks
STATE: California
COUNTRY: USA
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Best Local Similarity
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100.0%; Pred. No. 2.4e-186;
ative 0; Mismatches 0;
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APPLICANT: Boyle, William
APPLICANT: Boyle, David
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin version 3.1
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Patent No. 6790833
GENERAL INFORMATION:
APPLICANT: Simonet, Scott
APPLICANT: Sarosi, Ildiko
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: PREVENTION AND TREATMENT OF CARDIOVASCULAR DISEASES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/064,832
FILING DATE:
                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 2085; DB 4; Best Local Similarity 100.0%; Pred. No. 2.4e-186; Matches 380; Conservative 0; Mismatches 0;
     APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE RFFERENCE: A-378 Rev
CURRENT APPLICATION NUMBER: US/08/577,788C
CURRENT FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 58
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STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
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SEQ ID NO 56
LENGTH: 401
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-577-788C-56
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US-09-064-832-2
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262 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
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100.0%; Pred. No. 2.4e-186;
cive 0; Mismatches 0;
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APPLICANT: Boyle, William
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TILE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378 Rev
CURRENT APPLICATION NUMBER: US/08/577,788C
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin version 3.1
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GENERAL INFORMATION: APPLICANT: Boyle, William APPLICANT: Lacey, David APPLICANT: Calzone, Frank
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Pred. No. 8.5e-186;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09072993C Patent No. 6346388
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Best Local Similarity 99.7
Matches 379; Conservative
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US-09-072-993C-1
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Patent No. 6297022

GENERAL INFORMATION:
APPLICANT: McDonnell, Peter C.
APPLICANT: Young, Peter R.
APPLICANT: Zou, Jun
ITILE OF INVENTION: A Method of Identifying Agonists and
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BRILER REPREMENCE: GHOOF INVENTION NUMBER: 60/061,334

BARLIER APPLICATION NUMBER: 60/061,334

BARLIER PILLING DATE: 1997-10-08

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 3.0
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0; Mismatches 0;
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Pred. No. 8.5e-186;
0; Mismatches 1;
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Conservative C
                 REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ 1D NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 401 amino acids TYPE: amino acid
   Winter, Robert B.
                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 380; Conservative
                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-064-832-2
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ORGANISM: Human
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APPLICANT: Michael R. Brigham-Burke
APPLICANT: Michael R. Voung
TITLE OF INVENTION:
ANTAGONIST FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TITLE OF INVENTION:
TITLE OF INVENTION:
ANTAGONIST FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TITLE OF INVENTION NUMBER: US/09/072,993C
CURRENT FILING DATE: 1994-05-06
PRIOR PRILING DATE: 1997-08-13
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-08-29
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MOLECULE TYPE: protein
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CITY: Thousand Oaks
STATE: California
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ZIP: 91320-1789
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                                                                             301 SDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY
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                                                                                                                                                                                                                                                                                  Sequence 142, Application US/08706945D
Fatent No. 636927
GENERAL INFORMATION:
APPLICANT: Boyle, William
APPLICANT: Lacey, David
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR PAPLICATION NUMBER: 08/577,788
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PATENTIN VEXEION 3.1
SEQ ID NO 142
LIENGTH: 364
                                                                                                                                                        361 OKLFLEMIGNOVOSVKISCL 380
                                                                                                                                                                              382 QKLFLEMIGNQVQSVKISCL 401
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Matches 364; Conservative
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                                                                                                                                                                                                                                                      RESULT 13
US-08-706-945D-142
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                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.7%; Score 1828; DB 3;
86.3%; Pred. No. 2.4e-162;
tive 24; Mismatches 28;
GENERAL INFORMATION:
APPLICANT: Boyle, willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
                                                                                                                                                                                                      1: Amgen Inc.
1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Winter Robert B. REFERENCE/POCKET NUMBER: INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 401 amino acids
amino acid
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Matches 328; Conservative
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; Sequence 2, Application US/08795445A

RESULT 15 US-08-795-445A-2

RESULT 14 US-08-974-022-2 ; Sequence 2, Application US/08974022 ; Patent No. 6015938

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86.3%; Pred. No. 2.4e-162;
Live 24; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,445A FILING DATE:
            APPLICANT: BOYle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTBOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                     ADDRESSE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: Callfornia
COUNTRY: USA
ZIP: 91320-1789
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                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A-378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 86.3
Matches 328; Conservative
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MOLECULE TYPE: protein
US-08-795-445A-2
GENERAL INFORMATION:
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Search completed: November 15, 2004, 19:02:06 Job time : 49 secs

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                                                                                                                     November 15, 2004, 18:54:37; Search time 145 Seconds (without alignments) 927.250 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-676-358-1
US-01-142-658-2
US-09-405-032-125
US-10-151-071-8
US-10-467-243-2
US-10-676-358-6
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US-10-232-858-4

5 US-10-785-109-4

5 US-10-785-114-4

US-09-062-113-106
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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DB seq length: 2000000000
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Perfect score:
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Sequence 106, App Sequence 5, Appli Sequence 1, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6,	#1.30
US-10-785-109-106 US-10-785-114-106 US-09-062-113-5 US-110-039-785-5 US-10-056-209-1 US-10-056-209-1 US-10-056-209-1 US-10-164-594-2 US-10-164-594-2 US-10-183-091-1 US-10-183-091-1 US-10-183-091-1 US-10-183-091-1 US-10-183-091-1 US-10-183-091-1 US-10-183-114-5 US-09-062-113-64 US-09-062-113-64 US-09-062-113-65 US-10-232-858-65 US-10-232-858-65 US-10-232-858-65 US-10-232-858-65 US-10-232-858-65 US-10-232-858-109-65 US-10-785-109-65 US-10-785-109-66	ALIGNMENTS ation US/09405032 i; gen Inc. TTION: OSTEOPROTEGERIN TTION: OSTEOPROTEGERIN TS. AMGENS: S: AMGENS: S: AMGEN Inc. S: AMGEN Inc. S: AMGEN Inc. United States United States United States S: AMGEN Inc. SETEM: PC-DOS/MS-DOS PRE: Ploppy disk IMP PC compatible SYSTEM: PC-DOS/MS-DOS PATION: AMMER: US/09/405,032 TTE: 24-Sep-1999 ATION: Chuknown> INFORMATION: INFORMATION: INFORMATION: INFORMATION: INFORMATICS: SO amino acids SO amino acids SO amino acids INFORMATICS: Do NO: 139: CTERISTICS: SO acid ESS: single Linear PROTEIN: SEQ ID NO: 139:
44444000000	n US/094050; 07827A1 Inc. Inc. Inc. Inc. Inc. Inc. Inc. Inc.
3991 4011	199, Application US/09405 19, Application US/09405 18 No. US20030207827A1 18 No. US20030207827A1 18 CANT: Amgen Inc. 18 CANT: Amgen Inc. 18 CF SEQUENCES: 168 18 ESPONDENCE ADDRESS: ADDRESSE: Amgen Inc. CITY: Thousand Oaks STREET: 1840 Dehavilla CITY: Thousand Oaks STREET: 1910 Dehavilla COUNTRY: United States ZIP: 91320 UTTER READABLE FORM: MEDIUM TYPE: Floppy di CMEDIUM TYPE: Floppy di CMEDIUM TYPE: Floppy di CMEDIUM TYPE: Floppy di CMEDIUM TYPE: 1840 Compa OPERATING SYSTEM: PC-D SOFTWARE: PATENTIN Rel- APPLICATION NUMBER: US, FILING DATE: 24-569-19 CLASSIFICATION: AUNCHON RNEY/AGENT INFORMATION: RNEY/AGENT INFORMATION: RNEY/AGENT INFORMATION: RNEY/AGENT INFORMATION: RNEY/AGENT INFORMATION: TOPOLOGY: 11near CULE TYPE: protein 120
	1-139 9, Application Of Department of Depart
	1139 10. Appli 1
200799999999999999999999999999999999999	1 105-032-139 ence 139, Application US/0940 ication No. US20303207827A1 NBEAL INFORMATION: APPLICANT: Amgen Inc. TITLE OF INVENTION: OSTEON NUMBER OF SEQUENCES: 168 CORRESPONDENCE ADDRESS: ADDRESSE: Amgen Inc. STREET: 1840 Dehavill CITY: Thousand Oaks STATE: California COUNTRY: United State ZIP: 91320 COMPUTRY: United State ZIP: 91320 COMPUTRY: Ink PC comp OPERATING SYSTEM: PC- SOFTWARE: PatentIn Re CURRENT APPLICATION NUMBER: UF FILING DATE: 48-680-11 CLASSIFICATION NUMBER: UF FILING DATE: 48-680-11 CLASSIFICATION CONCETT REFERENCE/POCKET NUMB FORMATION FOR SEQ ID NO: 139: SEQUENCE CHRACTERISTICS: LENGTH: 380 amino acid TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein TOREGREENTE TYPE: DESCRIPTION: SEQ
11111110000000000000000000000000000000	RESULT 1 US-09-405-032-139 Sequence 139, A Publication No. GENERLI INFORMATION FILE OF CORRESPO CORRESPO STA COMPUTER CIT CIT CIT COMPUTER
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RESULT 3
US-10-142-658-2
US-10-142-658-2
; Sequence 2, Application US/10142658
; Publication No. US20030022834A1
; GENERAL INFORMATION:
; APPLICANT: Scatena, Marta M.
; APPLICANT: Scatena, Marta M.
; APPLICANT: Scatena, Marta M.
; TITLE OF INVENTION: METHODS AND DEVICES FOR PROMOTING ENDOTHELIAL MORPHOGENESIS
; TITLE OF INVENTION: METHODS AND US/10/142,658
; CURRENT APPLICATION NUMBER: US/10/142,658
; CURRENT APPLICATION NUMBER: US 60/290,230
; RIOR APPLICATION NUMBER: US 60/290,230
; RIOR FILING DATE: 2002-05-09
; NUMBER OF SEQ ID NOS: 2
; SOPID NO 2
; SEQ ID NO 2
; SED ID NO 2
; TITLE OF METHODS AND SCATENA METHODS A
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Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0;
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ORGANISM: Homo Sapiens
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100.0%; Score 2085; DB 16; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.9e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0;
                                                                                                     ô
                                               Length 380;
                                                                                                     Indels
                                               ; Score 2085; DB 10;
; Pred. No. 2.9e-167;
0; Mismatches 0;
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TITLE OF INVENTION: Osteoprotegerin in Milk
FILE REFERENCE: 8826-6852
CURRENT APPLICATION NUMBER: US/10/676,358
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: W0 2002 EP 02912
PRIOR APPLICATION NUMBER: EP 20010108414
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 380
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                                                       100.0%;
100.0%;
                                                          Query Match
Best Local Similarity 100.
Matches 380; Conservative
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US-10-676-358-1
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Matches 380; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                             SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV
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                                                                                                                                                                                                      ZIP: 91320
COMPUTER READABLE FORM:
DIDN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378-CIP2
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/405,032
FILING DATE: 24-Sep-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 125:
                                                                                                                  ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States
                                                APPLICANT: Amgen Inc.
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 168
CORRESPONDENCE ADDRESS:
Sequence 125, Application US/09405032
Publication No. US20030207827A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 380; Conservative
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RESULT 5
US-10-151-071-8
US-10-151-071-8
; Sequence 8, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV
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APPLICANT: ANDERSON, Dirk
TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
FILE REFERENCE: 3277-A
CURRENT APPLICATION NUMBER: US/10/151,071
CURRENT FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/291,919
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2085; DB 14;
100.0%; Pred. No. 3.1e-167;
iive 0; Mismatches 0; :
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; Sequence 2, Application US/10467243
; Publication No. US20040132971A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Holdings Ltd.; APPLICANT: Haning, Useper Mortensen
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
; FILE REFERENCE: 022600310
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CURRENT APPLICATION NUMBER: US/10/467,243
CURRENT FILING DATE: 2003-08-06
FRIOR APPLICATION NUMBER: US PA 2001 00214
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-09
FRIOR PELING DATE: 2001-03-09
FRIOR PILING DATE: 2001-03-29
FRIOR FILING DATE: 2001-03-23
FRIOR APPLICATION NUMBER: US 60/278,320
FRIOR FILING DATE: 2001-03-23
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LENGTH: 401
TYPE: PRT
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300

457

240 397

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APPLICANT: HIGASHION Kanji
TITLE OF INVENTION: No. US20020051969Alel Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                          SDQILKILSEMRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
278 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 337
                                                                                                                                                                                                                                                                       458 SDQILKILISIMRIKNGDQDTIKGIMHALKASKTYHFPKTVTQSLKKTIRFLASFTMYKLY 517
                                                                                            241 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP
                                                                                                                                                                                 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN
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MOCHIZUKI, Shin'ichi
YANO, Kazuki
KOBAYASHI, Fumie
SHIMA, No. US20020051969Aluyuki
YASUDA, Hisataka
NAKAGAWA, No. US20020051969Aluaki
NAKAGAWA, No. US20020051969Aluaki
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PRIOR APPLICATION DATA:
PREDELICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 207508/1995
APPLICATION NUMBER: UP 207508/1995
FILING DATE: 21-JUL-1995
PRIOR APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
PRIOR APPLICATION NUMBER: US 08/915,004
PRIOR APPLICATION NUMBER: US 08/915,004
APPLORIVATION NUMBER: US 08/915,004
ATTORNEY AGENT INFORMATION:
NAME: MOORE, ROADA P.
REGISTRATION NUMBER: 44,244
REFREENCY AGENT NUMBER: 44,244
REFREENCY NUMBER: 44,244
REFREENCY NUMBER: AND 0500V
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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125 High St.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,113
                                                                                                                                                                                                                                                                                                                                                               518 QKLFLEMIGNQVQSVKISCL 537
                                                                                                                                                                                                                                                                                                                                  361 OKLFLEMIGNOVOSVKISCL 380
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APPLICANT:
APPLICANT:
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APPLICANT:
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US-09-062-113-4
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                                                                                                                                                                                                                                                     61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
                                                                                                                                                                                                                                                                                       82 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 141
                                                                                                                                                                                                                                                                                                                                                                 142 CKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 CEEAFFRFAVPTKFTPNMLSVLVDNLPGTKVNAAESVERIKRQHSSQEQTFQLLKLWKHQN
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                                                                            Length 401;
                                                                                                                       0; Indels
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US-10-676-358-6
                                                                            100.0%; Score 2085; DB 16;
100.0%; Pred. No. 3.1e-167;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL TREASMENT NESTEC SA TITLE OF INVENTION: Osteoprotegerin in Milk FILE REPERRNET 8826-5852
CURRENT APPLICATION NUMBER: US/10/676,358
CURRENT PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: WC 2002 EP 02912
PRIOR FILING DATE: 2003-03-15
PRIOR RILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 537
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                                                                                                                           Matches 380; Conservative
                  ; ORGANISM: Homo sapiens
US-10-467-243-2
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Best Local Similarity
Matches 380; Conserv
                                                                                                     Best Local Similarity
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US-10-676-358-6
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APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: YANO, Kazuki
APPLICANT: SHOAYASHI, Fumie
APPLICANT: SHIMA, Nobuyuki
APPLICANT: SHIMA, Nobuski
APPLICANT: WAKAGAWA, Nobuski
APPLICANT: WAKAGAWA, Nobuski
APPLICANT: UEDA, Masatsugu
APPLICANTON NUMBER: US 00/232,858
PRIOR PILING DATE: 1996-02-20
PRIOR PILING DATE: 1996-02-20
PRIOR PILING DATE: 1996-02-20
PRIOR PILING DATE: 1996-02-20
PRIOR FILING DATE: 1995-02-20
PRIOR FILING DATE: 1995-02-20
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn version 3.1
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Pred. No. 9.4e-167;
0; Mismatches 1; Indels 0
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Publication No. US20040142426A1
GENERAL INFORMATION:
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APPLICANT: TSUDA, Eisuke
APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: KOBAYASHI, Fumie
APPLICANT: SHIMA, Nobuyuki
         SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
INGITH: 380
TYPE: PRT
                                                                                                                                                                      Query Match
Best Local Similarity 99.7%;
Matches 379; Conservative
                                                                                                  ; ORGANISM: Homo sapiens
US-10-232-858-4
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APPLICANT: TSUDA, Eisuke
APPLICANT: TSUDA, Eisuke
APPLICANT: WOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: WASUANA: Fumie
APPLICANT: SHIMA, NO. US20030153048Aluyuki
APPLICANT: SHIMA, NO. US20030153048Aluyuki
APPLICANT: YASUDA, Hisataka
APPLICANT: TASUDA, Hisataka
APPLICANT: WAKAGAWA, NO. US20030153048Aluaki
APPLICANT: UEDA, Masatsugu
APPLICANT: UEDA, Masatsugu
APPLICANT: UEDA, Masatsugu
APPLICANT: NO. US20030153048Alel Proteins and Methods for Producing the Prot
CURRENT FILING NATE: 1091.004
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: PCT/JP96/00374
PRIOR PPLICATION NUMBER: PCT/JP96/00374
PRIOR APPLICATION NUMBER: 08/915,004
PRIOR FILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 108
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signal peptide)"
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Pred. No. 9.4e-167;
0; Mismatches 1;
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Publication No. US20030153048A1
                                                                                                                                                                                                                                                                                                                                              99.7%;
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                   380 amino acids
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.7
Matches 379; Conservative
                                                                                                                                                     MOLECULE TYPE: protein FEATURE:
                                                                                                                                                                                                                             LOCATION: 1..380
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                   NAME/KEY: Protein
                                                                                      TYPE: amino acid STRANDEDNESS:
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                                                                   LENGTH:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 379; Conserv
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CITY: Boston
STATE: MA
COUNTRY: USA
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US-09-062-113-106
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US-10-785-114-4
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CURRENT APPLICATION NUMBER: US/10/785,114
CURRENT FILING DATE: 2004-02-25
PRIOR PRILING DATE: 2002-09-03
PRIOR PRILING DATE: 1997-08-20
PRIOR FILING DATE: 1999-03
PRIOR FILING DATE: 1999-03
PRIOR FILING DATE: 1999-02-20
PRIOR APPLICATION NUMBER: PCT/JP96/00374
PRIOR FILING DATE: 1995-07-21
PRIOR FILING DATE: 1995-03-30
PRIOR FILING DATE: 1995-03-40
PRIOR FILING DATE: 1995-03-40
PRIOR FILING DATE: 1995-03-50
PRIOR FILING DATE: 1995-03-40
PRIOR FILING DATE:
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                                                                                                                            Length 380;
                                                                                                                                                                                   1; Indels
                                                                                                                                 Score 2079; DB 16;
Pred. No. 9.4e-167;
0; Mismatches 1;
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T: TSUDA, Bisuke
T: MOCHIZUKI, Shin'ichi
T: YANO, Kazuki
T: KOBAYASHI, Fumie
T: SHIMA, Nobuyuki
T: YASUDA, Hisataka
T: NAKAGAWA, Nobuaki
T: MORINAGA, TOMONOYI
                                                                                                                                      99.7%;
                                                                                                                                         Query Match
Best Local Similarity 99.7
Matches 379; Conservative
                                    TYPE: PRT
CRGANISM: Homo sapiens
US-10-785-109-4
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US-10-785-114-4
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APPLICANT: UEDA, Masatsugu
APPLICANT: UEDA, Masatsugu
APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: No. US20020051969Alel Proteins and Methods for Producing
TITLE OF INVENTION: the Proteins
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
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                                                                                                                           1 ETPPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                                                                                                                                                                          61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLLEIEFCLKHRSCPPGFGVVQAGTPERNTV
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                                                                                             1 ETFPRKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                               Gaps
                                               ;
     Length 380;
                                               Indels
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APPLICATION NUMBER: US/09/062,113 FILING DATE: 17-APR-1998
99.7%; Score 2079; DB 16;
99.7%; Pred. No. 9.4e-167;
iive 0; Mismatches 1;
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APPLICANT: GOTO, Masaaki
APPLICANT: TSUDA, Eisuke
APPLICANT: TSUDA, Eisuke
APPLICANT: MOCHIZUKI, Shin'ichi
APPLICANT: YANO, Kazuki
APPLICANT: SHIMA, No. US20020051969Aluyuki
APPLICANT: SHIMA, No. US20020051969Aluyuki
APPLICANT: YASUDA, Hisataka
APPLICANT: YASUDA, Hisataka
APPLICANT: MORINAGAWA, No. US20020051969Aluaki
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CLASSIFICATION:
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: JP 54977/1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                       Conservative
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Sequence 106, Application US/10785109
Publication No. US20040142426A1
GENERAL INFORMATION:
APPLICANT: GOTO, Masaaki
APPLICANT: TSUDA, Eisuke
APPLICANT: MOCHZUKI, Shin'ichi
APPLICANT: KOBAYASHI, Fumie
APPLICANT: SHIMA, Nobuyuki
APPLICANT: SHIMA, Nobuyuki
APPLICANT: YASUDA, Hisataka
APPLICANT: MAKAGAWA, Nobuski
APPLICANT: MAKAGAWA, Nobuski
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PRIOR FILLING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: US 08/915,004
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          Kanji
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Best Local Similarity 99.7
Matches 379; Conservative
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US-10-232-858-106
        HIGASHIO,
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99.7%; Score 2079; DB 9; Length 391;
Best Local Similarity 99.7%; Pred. No. 9.7e-167;
Matches 379; Conservative 0; Mismatches 1; Indels
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MOCHIZUKI, Shin'ichi
YANO, Kazuki
KOBAYASHI, Fumie
SHIMA, No. US20030153048Aluyuki
YASUDA, Hisataka
NAKAGWA, No. US20030153048Aluaki
MOKRAGWA, Tomonori
UEDA, Masatsugu
                                                                                      APPLICATION NUMBER: PCT/JP96/00374
FILING DATE: 20-FEB-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,004
FILING DATE: 20-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: MOORE, ROADA P.
REGISTRATION NUMBER: 44,244
REFRENCE/DOCKET NUMBER: FUN-060DV
TELEPHONE: (617) 248-7000
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: G17) 248-7100
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                                                      21-JUL-1995
20-FEB-1995
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amino acid
                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-062-113-106
              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 21-JUL-
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: No. US20030153048Alel Proteins and Methods for Producing the Proteins RILE REFERENCE: 1699, 004
CURRENT APPLICATION NUMBER: US10/232,858
CURRENT FILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: PCT/JP96/00374
PRIOR APPLICATION NUMBER: PCT/JP96/00374
PRIOR APPLICATION NUMBER: 06/915,004
PRIOR RILING DATE: 1997-08-20
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 106
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APPLICANT: HIGASHIO, Kanji
TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
FILE REFERENCE: 16991.017
CURRENT APPLICATION NUMBER: US/10/785,109
CURRENT FILING DATE: 2004-02-25
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Pred. No. 9.7e-167;
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TYPE: PRT
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PRIOR FILING DATE: 1997-08-20
PRIOR APPLICATION WUMBER: PCT/JP96/00374
PRIOR PILING DATE: 1996-02-20
PRIOR FILING DATE: 1995-07-21
PRIOR FILING DATE: 1995-07-21
PRIOR FILING DATE: 1995-07-21
PRIOR FILING DATE: 1995-02-20
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
LENGTH: 391
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ORGANISM: Homo sapiens
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US-10-785-109-106
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                                                                                                                                                                                                                                                                                                                               12 BTFPPRYLHYDBBTSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHXYTDSWHTSDBCL
                                                                                                                                                                                                                                                                                                       1 ETFPPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECL
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                  Length 391;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                Score 2079; DB 16;
Pred. No. 9.7e-167;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November 15, 2004, 19:04:37 Job time: 147 secs
                                                         054977/1995
                    207508/1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 OKLFLEMIGNOVOSVKISCL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 OKLFLEMIGNOVOSVKÍSCL 391
PRIOR FILING DATE: 1996-02-20
PRIOR APPLICATION NUMBER: JP 207.
PRIOR FILING DATE: 1995-07-21
PRIOR APPLICATION NUMBER: JP 054!
PRIOR FILING DATE: 1995-02-20
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 106
                                                                                                                                                                                                                                      99.78;
                                                                                                                                                                                                                                                        Best Local Similarity 99.7
Matches 379; Conservative
                                                                                                                                                                                 ORGANISM: Homo sapiens
US-10-785-114-106
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GenCore version 5.1.6
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                 Copyright
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sw model using OM protein - protein search, November 15, 2004, 18:50:46; Search time 39 Seconds (without alignments) 937.497 Million cell updates/sec Run on:

US-10-676-358-1 2085 Perfect score:

1 BIFPPRYLHYDEETSHQLLC.....QKLFLEMIGNQVQSVKISCL 380 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
(: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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26	വല്യ		277 595	000	I37552 A42086	homolog antigen
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hypothetical prote	protein 722A3 8 (i	hypothetical prote	laminin alpha chai	serine profeinase	hypothetical prote	OCCUST Wall profes	laminin beta-1 cha	laminin beta-1 cha	protein-tyrosine k	fibrillin-2 precur	subtilisin-like or	Subtilisin-like or	laminin alcha-1 ch	hypothetical prote	laminin beta-1 cha
T25473	F87908	T23064	T43291	S34583	T33383	836016	MMHUB1	MMFFB1	870713	A54105	G02428	JC6148	S18253	T20968	MMMSB1
N	~	7	N	7	N	N	7	Н	7	~	N	~	7	7	Н
643	2823	2823	3102	1548	398	1252	1786	1790	1369	2918	899	915	3712	2610	1786
6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.2	6.2	6.2	6.2	6.2	6.1	6.1	6.1
136.5	135.5	135.5	135.5	135	134	133	132.5	130	129.5	129.5	128.5	128.5	128	127.5	126.5
		32					37	_	_						

ALIGNMENTS

148854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C; Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004
C;Accession: I48854
10.00 th 11.00 th 11.

RESULT 1

R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: 14884, MUID:95178848; PMID:7873884
A;Reference number: 148854
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Rossidues: 1-459 <RES>
A;Cross-references: UNIPROT:Q62327; EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:943383:C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homology F;151-188/Domain: NGF receptor repeat homology <NGF>

9 Query Match
Best Local Similarity 35.7%; Pred. No. 1.7e-15;
Matches 74; Conservative 23; Mismatches 85; Indels 25.

89 DQVETRACTKQQNRVCACBAGRYCALKTHSGSCRQCWRLSKCGPGFGVASSRAPNGNVLC 148 122 KRCPDGFFSNETSSKAPCRKHINCSVFGLLITQKGNATHDNICSGNSESTQKCGIDVTLC 181 --CLKHRSCPPGFGVVQAGTPERNTVC 121 89 88 9 HYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 69 LQYVKQECNRTHNRVCECKEGRYLEIEF----셤 δ à g ò

---YVSQPEPTRSQP----LDQEPG 219 182 EEAFFRFAVPTKFTPNWLSVLVDNLPG 208 202 à g

셤

RESULT B38634

tumor necrosis factor receptor type 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: B38634; A40254; S54816
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.)
Proco. Natl. Acad. Sci. US.A. 88, 2830-2834, 1991
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Mocession: B38634
A;Molecule type: mRNA
A;Residues: 1-474 <LEW>

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A; Accession: B35010
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N.Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2

C.Species: Homo sapiens (man)

C.Species: Homo application (man)

S.Species: As a sapient (man)

A.Species: A receptor for tumor necrosis factor defines an unusual family of cellular and

A.Reference number: A35356, MUD:90260639; PMID:2160731

A.Accession: A35356

A.Stelence: Lype: mRNA

A.Molecule type: MR
A;Cross-references: UNIPROT:P25119; GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type I and type 2 murine receptors for A;Title: Molecular cloning and expression of the type I and type 2 murine receptors for A;Reference number: A40254 MUID:91246168; PMID:1645445
A;Accession: A40254
A;Accession: A40254
A;Residues: 1-474 <GGO>
A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Pellower, R.; Peldmann, M.; Chernajovsky, Y.
Submitted to the EMBL Data Library, May 1995
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
A;Residues: Dreliminary
A;Molecule type: DMA
A;Residues: Dreliminary
A;Molecule type: DMA
A;Residues: 1-22 <KIS>
A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Stymorfamily: tumor necrosis factor receptor type 2 (TRFR2); NGF receptor repeat homology colin F;1-22/Domain: NGF receptor repeat homology <MG2>
F;1-22/Domain: NGF receptor repeat homology <MG2>
F;79-120/Domain: NGF receptor repeat homology <MG2>
F;166-203/Domain: NGF receptor repeat homology <MG2>
F;166-203/Domain: NGF receptor repeat homology <MG3>
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A; Cross-references: GB: M55994; GB: M38549; NID: g339757; PIDN: AAA36755.1; PID: g339758
R; Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 LOYVKQECHRTHNRVCECKEGRYLEIBF-----CLKHRSCPPGFGVVQAGIPERNTVC 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 KACAPGTFSDTTSSTDVCRPHRICSILAI----PGNASTDAVCA--PESPTLSAIPRTL- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 HYDBETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKE 68
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Best Local Similarity 35./*
The TA; Conservative
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A;Molecule type: mRNÅ; protein
A;Residues: 23-461 cDEM>
A;Residues: 23-461 cDEM>
A;Cross-references: GB:S63368; NID:g235649; PIDN:AAB19824.1; PID:g235649
A;Cross-references: GB:S63368; NID:g235649; PIDN:AAB19824.1; PID:g235649
A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
B;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstrat A;Reference number: A36007; MUID:90349572; PMID:2166946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 116-140, 'P',142-195,'R',197-362,'T',364-461 <HEL>
A; Cross-references: GB:M35857; NID:g339751; PIDN:AAA63262.1; PID:g339752
R; Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
A; Title: Purification and partial anno acid sequence analysis of two distinct tumor nec A; Reference number: A23666; MUID:91056048; PMID:2173696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kuhnert, P.; Kemper, O.; Wallach, D.
Andrea 150, 381-386, 1984
A;Title: Cloning, sequencing and partial functional characterization of the 5' region of A;Title: Cloning, sequencing and partial functional characterization of the 5' region of A;Reference number: 138094; WUID:95121934; PMID:7821811
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A;Note: the list of introns is incomplete
B;Note: the list of introns is incomplete
C;Superfamily: fumor necrosis factor receptor; transmembrane protein
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
B;1-22/Domain: signal sequence #status predicted <SIG>
B;2-346/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
B;40-76/Domain: NGF receptor repeat homology <NGI>
B;78-119/Domain: NGF receptor repeat homology <NGI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Residues: 23-40,65-69;136-141;300-306 <LOE>
R, Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A, Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A, Reference number: A35010; MUID:90110215; PMID:2153136
Cytokine 2, 231-237, 1990
A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A;Reference number: A48416; MUID:91370690; PMID:1966549
A;Accession: A48416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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F;164-201/Domain: NGF receptor repeat homology <NG4>
F;164-201/Domain: Under receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracellular #status predicted <INT>
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: 138094
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A,Cross-references: GDB:125914; OMIM:191191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1p36.2-1p36.2
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A; Residues: 27-31 < ENG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
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A Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Cross-references: GB: M3312; NID: g1553058; PIDN: AAB08705.1; PID: g1553059; GB: M94126; N1
A; Experimental source: BALB/c, liver
A; Note: sequence extracted from NCBI backbone (NCBIP: 120357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        partial amino acid seguence of the receptor-like
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A;Map position: 20q12-20q13.2
C;Superfamily: CD27 antigen; MGF receptor repeat homology
C;Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <81G>
F;21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
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A;Title: Biochemical characteristics and partial amino acid sequence of the receptor-like A;Reference number: A60771; MUID:89093941; PMID:2463309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
BMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor A;Reference number: S04460; MUID:89356608; PMID:2475341
A;Accession: S04460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 SPVCKELQYVKQECNRTHNRVCECKEGRYL---BIBFCLKHRSCPPGFGVVQAGTPERNT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCKRCPDGFFSNETSSKAPCRKHINCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 LCEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 NKAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----QDPQEMEDYPGHNTAA-PVQETLHGCQ 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 QYLHDGQ-----сcbicQPGSRIJSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 VCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKGTSQTNVICGLKSRMRALLVIPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Homo sapiens (man)
C.Date: 03-Jun_1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 KYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC---LYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                 13.6%; Score 284.5; DB 2; Length 27.3%; Pred. No. 3.6e-12; Live 37; Mismatches 109; Indels
                                                                                                                                                                                                                       C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>
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A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GILITIFGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B-cell activation protein CD40 precursor - hum: N;Alternate names: B-cell surface antigen Bp50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.6%
Best Local Similarity 27.3%
Matches 83; Conservative
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A; Residues: 1-277 <STA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 PVTQ 264
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C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q98SM6; GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
tresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B cell-associated suxface molecule CD40, long splice form - mouse (5,Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46476; A46515
R;Torres, R.M.; Clark, E.A.
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine A;Reference number: A46476; MUID:92105763; PMID:1370315
A;Accession: A46476
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A/Cross-references: UNIPROT:P27512; GB:M83312; NID:g1553058
A/Cross-references: UNIPROT:P27512; GB:M83312; NID:g1553058
A/Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
B/Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992
A/Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A/Reference number: A46515; MUID:93094586; PMID:1281194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;1-21/Domain: signal sequence #status predicted <SIG>
;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
;332-350/Domain: transmembrane #status predicted <TMM>
;410-475/Domain: death domain #status predicted <ADD>
;551-651/Region: conserved cytoplasmic #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
                                                                                                                                                                                                      death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                             C; Accession: JC7705
R; Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A; Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A; Reference number: JC7705; MUID:21308433; PMID:11414698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 KYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 CKELQYVKQECNRTHNRVCECKEGRYLBIBFCLKHRSCPPGFGVVQAGTPERNTVCKRCP
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RCPDGFFSNEISSKAPCRKHINCSVFGLLLIQKGNAIHDNICSGNS 168
                                         PCAPGIFSNITSSIDICRPHQICNVVAI----PGNASMDAVCTSIS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Mismatches 105; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 TY--EAPPTAYLPKGLNSSVFDLSSSPAPRVSNGTAE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.5%; Score 322.5; DB 2 31.8%; Pred. No. 2.2e-14;
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-651 <BRI>
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A,Cross-references: UNIPROT:P34015; EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g43910
A,Experimental source: strain Bangladesh 1975
C,Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:P34015; GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
A;Experimental cv. A.; Bilnov, VM.; Gytorov, VV.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frol submitted to the EMBL Data Library, April 1999
A;Description: Nucleotide sequence analysis of the region of Variola virus Xhol F O H P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPVCKELQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GDVIČSPČGFGTYSHTVSSADKČEPVPNNTFNYIDVEITLYPVNDISCTRTTTTGLSESI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
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A;Residues: 1-39 <KOD>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Cross-references: Exain India-1967, isolate Ind3
B;Experimental source: strain India-1967, isolate Ind3
B;Experimental source: strain India-1967, isolate Ind3
B;Experimental source: strain India-1967, isolate Ind3
B;ERBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the hc
A;Reference number: S32385; MUID:93202281; PMID:8384129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 NGRCNSNQVETRSCNTTHNRICECSPGYYCLLKGSSGCKACVSQTKCGIGYG-VSGHTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 RNIVCKRCPDGFFSNEISSKAPCRKHINCSVFGLLLIQKGNAIHDNIC----SGNSESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | : | : | : | : | : | : | : | EYFSVINKVATSGFFTGENRYQNISK------VCTLNFEIKCNNKGSSFKQLTKAKND-
                                                                                                                                                                                                                                                                                                                                                  4 PPKYLHYDEE-TSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 QKCGIDVTL----CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTFQLLK-----LWKHQNKAQDIVKKIIQDIDLCENSVQRHIGHANLTFFQLRSLMESL
                                                                                                                                                                                                                                                                                                                                                                                                                                  26 PPNGKCKÖTÉYKRÜNÍCCLSCPPGTYASRLCDSKTNÍQCTPCGSGTFÍSRNNHLPACLSC
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                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                          Length 348;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                     ; Score 232.5; DB 2;
; Pred. No. 1.4e-08;
47; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Readdues: 31-168 <5HC>
A;Cross-references: ENRBL:X69198
A;Experimental source: strain India-1967, ssp. major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Date: 30-Sep-1993 #sequence revision 30-Sep-1993 C,Accession: D36858; S46888; S32385; S35987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTSELTITMNHTDCNPVF-----
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N;Alternate names: B28R protein (COP)
C;Species: variola virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R.Blinov, V.M. submitted to GenBank, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---KTVTQSLKKTIRFL 351
                                                                                                                                                                                              Query Match
Best Local Similarity 23.6%;
Matches 89; Conservative 4'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A36859
A;Accession: D36858
A;Residues: 1-348 <MAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Accession: S32385
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Cipate: 24-May-1996 #text_change 09-Jul-2004
Cipate: 24-May-1996 #text_change 09-Jul-2004
Cipate: 24-May-1996 #text_change 09-Jul-2004
Cipate: 24-May-1996 #text_change 09-Jul-2004
Cipatession: 154182
Airtie: Construction and evaluation of a hncDNA library of human 12p transcribed sequent Airtie: Construction and evaluation of a hncDNA library of human 12p transcribed sequent Airtie: Construction and evaluation of a hncDNA library of human 12p transcribed sequent Airtie: Construction and evaluation of a hncDNA library of human 12p transcribed sequent Airtie: Construction and evaluation of a hncDNA library of human 12p transcribed sequent Airtie: Construction and evaluation GB/EMBL/DDBJ
Airtie: Construction GB/EMBL/DDBJ
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hypothetical protein G2R - variola major virus

hypothetical protein G2R - variola major virus

C;Species: variola major virus

C;Species: variola major virus

C;Species: variola major virus

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T28623

R;Massung, R.F; Esposito, J.J; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin

Nature 366, 748-751, 1993

A;Title: Potential virulence determinants in terminal regions of variola smallpox virus

A;Reference number: Z20488; MUID:94088747; PMID:8264798

A;Accession: T28633

A;Accession: T286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 KQ--ECNRTHNRVCECKEGRY----LBIEFCLKHRSCPPGF-GVVQAGTPERNTVCKRC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 YCDPNLG--LRVQQKGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIAIGVS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YCSPVCKELQYVKQECNRTHNRVCECKEGRYL---EIEFCLKHRSCPPGFGVVQAGTPER 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 ETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYV 72
                                                                                                                                                                                                                                                                                                                                                                       4 PPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDEC---L 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
C;Date: 24-May_1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                          PPTACREKQYLINSQCCSLCQPGQKLVSDCTEFTETECLPCGESBFLDTWNRETHCHQHK
                                                                                                                                                                                                                                                                                           Gaps
                                          F;194-215/Domain: transmembrane #status predicted <TVM>
F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 NTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215
                                                                                                                                                                                                          Length 277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                           80; Indels
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                                                                                                                                                                                                                   Score 264; DB 2;
Pred. No. 8.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.5%; Score 239.5; DB 2
Best Local Similarity 30.9%; Pred. No. 6.1e-09;
Matches 51; Conservative 21; Mismatches 84
                                                                                                                                                                                     12.7%; Sco...
33.5%; Pred. No. o...
23; Mismatches
                extracellular #status predicted
                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                               :99
            F;21-193/Domain:
                                                                                                                                                                                                                   Query Match
Best Local S
Matches 56
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T2 protein - rabbit fibroma virus
C;Species: rabbit fibroma virus
C;Species: rabbit fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Species: rabbit fibroma virus, Shope fibroma virus
C;Species: Dalange of the circle of the control of the co
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A;Rossidues: 1-326 c.VDT>
A;Rossidues: 1-326 c.VDT>
A;Rossidues: UNIPROT:P29825; GB:M95181; GB:M37976; NID:G332309; PIDN:AAA46632.1; 1
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
C;Keywords: glycoprotein
F;64-105/Domain: NGF receptor repeat homology <NG2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROF:P25943; GB:M17433
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
F;64-105/Domain: NGF receptor repeat homology <NG2>
F;106-147/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homology to the tumor necrosis
       172 QKCGIDVTL----CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQE 227
                                                                                                                                                                                                                                                   QTFQLLK-----LWKHQNKAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESL 281
                                                                                                                                                                                                                                                                                               226 EYFSVLNKVATSGFFTGENRYQNISK------VCTLNFEIKCNNKGSSFKQLIKAKND- 277
                                                                                                                                                                                                                                                                                                                                                                                            282 PGKKVGAEDIBKTIKA-CKPSDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFP--- 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 DGWMSHSETV--TLAGDCLSSVDIYILYSNTNAQDYETDTISYRVGNVLDDDS-HMPGSC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 RIHNRVCECKEGRYLEIE-----FCLKHRSCPPGFGVVQAGIPERNIVCKRCPDGFFSN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EISSKAPCRKHINCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTL----CEEAF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: myxoma virus
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 LLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.8%; Score 225; DB 2; Similarity 30.9%; Pred. No. 4.3e-08; 55; Conservative 22; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: A40566
R;Upton, C.; Macen, J.L.; Schreiber, M.; Mcfadden,
Virology 184, 370-382, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQVZML
T2 protein - myxoma virus (strain Lausanne)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335 DIHKLITNS--KPTRFL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---KTVTQSLKKTIRFL 351
                                                                                                                                                                            206 LISELTITMNHIDCNPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <UPT>
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Best Local S:
Matches 55
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R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Accession: D72175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: UNIPROT.P34015; GB:Y16780; NID:g5830555; PIDN:CAB54798.1; PID:g5830;
A.Experimental source: strain Garcia-1966
                                                         C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology F;32-66/Domain: NGF receptor repeat homology <NGF>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPVCKELQYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 QKCGIDVTL----CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 RNTVCKRCPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNIC-----SGNSEST 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 QTFQLLK-----LWKHQNKAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 DGMMSHSETV--TLAGDCLSSVDIYILYSNTNAQDYETDTISYRVGNVLDDDS-HWPGSC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: variola minor virus
Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PPKYLHYDEE-TSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYC
                                                                                                                                                                                                                                                                                                                                                                                                                                       PNGKCKDTEYKRHNLCCLSCPPGTYASRLCDSKTNTQCTPCGSGTFTSRNNHLPACLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 PGKKVGAEDIEKTIKA-CKPSDQILKLLSLWRIKNGDQDTLKGLMHALKHSKTYHFP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PPKYLHYDEE-TSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                83;
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                                                                                                                                                                                                                                            Length 349;
                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                             47; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G2R protein - variola minor virus (strain Garcia-1966)
                                                                                                                                                                                                                                                                                Pred. No. 1.4e-08
                                                                                                                                                                                                                                         11.2%; Score 232.5; 23.6%; Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 LTSELTITMNHTDCNPVF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 NIHKPITNS--KPTRFL 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 ---KTVTQSLKKTIRFL 351
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <SHC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                         Query Match
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C;Genetics:
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Matches
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A.Gross-references: UNIPROT:P08138; GB:M14764; NID:9189204; PIDN:AAB59544.1; PID:9189205 R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.; R. Neurochem. 48, 225-232, 1987 A; Title: Purification and amino terminal sequencing of human melanoma nerve growth factor A;Reference number: A60204; MUID:87085574; PMID:3025363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A;Residues: 29-31, T', 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A;Residues: 29-31, T', 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A;Residues: 29-31, T', 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A; Mole: this sequence has been corrected by a note added in proof to follow the nucleotic R; Vissavajihala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochen. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor recent an unber: $21689; MUID:92198017; PMID:1372492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A) Status: 10.000
A) Status: preliminary; translated from GB/EMBL/DDBJ
A) Status: preliminary; translated from GB/EMBL/DDBJ
A) Status: 1-22 cRES
A) CROSS-references: GB:M21621; NID:9189206; PIDN:AAA36363.1; PID:9189207
A) Cross-references: GB:M21621; NID:9189206; PIDN:AAA36363.1; PID:9189207
C) Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma C
C) Comment: This protein exich region of the extracellular domain may form part or all of C) Comment: This protein is thought to form a high-affinity receptor when it associates w
C) Comment: This receptor undergoes both N- and O-linked glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A hay postanily: nerve growth factor receptor; NGF receptor repeat homology.

C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
E;12-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <MAT>
F;29-257/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
                    Mercer, E.; Bothwell, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the nerve growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 YLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHY-YTDSWHTSDECLYCSPV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 YTHSGE-----CCKACNLGEGVAQPCGAN-QTVCEPCLDSVTFSDVVSATEPCKPCTE-
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F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                RiJohnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor. A;Reference number: A25218; MUID:87051725; PMID:3022937
                            Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 183-208 «VIS»
Mol. Cell. Bid. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the A;Meference number: 157638; MUID:89096903; PMID:2850491
A;Accession: 157638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 185.5; DB 1
Pred. No. 2.8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 CEECPDGTYSDBANHVDPCLPCTVC 170
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A,Cross-references: GDB:120234; OMIM:162010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CKRCPDGFFSNETSSKAPCRKHINC 145
C; Accession: A25218; A60204; S21689; I57638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;197-248/Region: serine/threonine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 17q21-17q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 48; Conserv
                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-427 < JOH>
                                                                                                                                                                                           A; Accession: A25218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haddle antigen 4-IBB precursor - mouse () Species: Mus musculus (house mouse) () Species: Musculus (house mouse) () Species: Musculus () Musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----CKTCSLGTF-NDONGTGV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                    78 RIHNRVCECKEGRYLEIE-----FCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 KTRDRVCDCSAGNYCLLKGQEGCRICAPKTKCPAGYG-VSGHTRTGDVLCTKCPRYTYSD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETSSKAPCRKHTN-CSV-FGLLLTQKGNATHDNICSGNSESTQKCGIDVIL----CEEAF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 AVSSTETČISSFNYISVERNÍZPV---NDÍSCITTAĞPNEVVKISEFSVILMHIDÖDPVF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                        predicted
                                                                                                                                                                                                                                                                         18 LLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECN 77
                                                                                                                                                                                                                                                                                                                                                       38 LCCTSCPPGSYASRLCGPGSDTVCSPCKNETFTASTNHAPACVSCRGRCTGHLSESOSCD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVCKELQYVKQECNRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 CDNCQPGTFCR-----KYNPVCKSCPPSTFS-SIGGQPNCNICR-VCAGYFRFKKFCSST
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nerve growth factor receptor precursor, low affinity [validated] - human N;Alternate names: NGF receptor C;Species: Homo sapiens (man)
                                            (covalent) #status
                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 256;
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                                                                                                                                                                                                    85; Indels
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            F;106-147/Domain: NGF receptor repeat homology <NG3>
F;66,181,205,238/Binding site: carbohydrate (Asn) (oc
                                                                                                                      10.5%; Score 219; DB 1;
30.6%; Pred. No. 1.1e-07;
iive 24; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 HNAECECIEGFHCLGPQCTRCEKDCRPGQELTKQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRKHTNCSVFGLLLTQKGNATHDNIC 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 32.28 Matches 47; Conservative
                                                                                                                                                           Similarity 30.6
55; Conservative
                                                                                                                                      / No.
Local Sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132
                                                                                                                                  Query Match
                                                                                                                                                                   Best Loca
Matches
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A;Molecule type: mRNA
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A;Crossidues: 1-461 **HINA
A;Crossidues: 1-461 **HINA
A;Crossidues: 1-461 **HINA
A;Crossidues: UNIPROT:P22934; GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
C;Keywords: duplication; AjvCoprotein; receptor; transmembrane protein
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-211/Domain: signal sequence #status predicted <EXT>
F;30-211/Domain: NGF receptor repeat homology <NG1>
F;44-82/Domain: NGF receptor repeat homology <NG3>
F;44-82/Domain: NGF receptor repeat homology <NG3>
F;44-126/Domain: NGB receptor repeat homology <NG3>
F;44-126/Domain: NGB receptor repeat homology <NG
                                                                                                                                                                                      C; Accession: B36555
R; Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; Ny Cell Biol. 9, 705-715, 1990
A; Title: Molecular cloning and expression of human and rat tumor necrosis factor recepted A; Reference number: A36555; MUID:91090841; PMID:1702293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 -NIVCKRCPDGFF--SNETSSKAPCRKHINCSVFGLLLIQKGNATHDN------ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 QNTVC-NCHAĞFFLSGNECTPCSHCKKNQEC--MKLCLPPVANVTNPQDSGTAVLLPLVI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 PGFNPTLGFSTTPRFSHPVSSTPISPVFGPSNWHNFVPPVREVVPTQGADPLLYGSLNPV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 FLGLCLLFFICISLLCRYPQWRPRVYSIICRDSAPVKEVEGEGIVTKPLTPASIPAFSPN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LSVLVDNLPGTK-----VNAESVERIKRQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 PIPARVRKWEDVVAAQPQRLDTADPAMLYAVVDGVPPTRWKEFWRLLGLSEHEIERLELQ 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 HSS--QEQTFQLLKLWKHQNKAQ----DIVKKIIQDIDL--CENSVQRHIGHANLTFEQL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----LENI 444
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-0un-1992 #sequence_revision 07-0ct-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #stetus predicted <NEM>
F:235-461/Domain: intracellular #stetus predicted <INT>
F:53-461/Domain: intracellular #stetus predicted <INT>
F:54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 KYLHYDEETSHQLLCDKCPPGTYLKQHCTAK-WKTVCAPCPDHYYTDSWHTSDECLYCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.9%; Score 185; DB 1; Length 461;
Best Local Similarity 20.9%; Pred. No. 3.3e-05;
Matches 89; Conservative 47; Mismatches 116; Indels 174; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ICSGNSESTQ------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :||
RETLES 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 ----
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Search completed: November 15, 2004, 19:01:13 Job time : 40 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

November 15, 2004, 18:38:30 ; Search time 192 Seconds Run on:

(without alignments) 1138.762 Million cell updates/sec

US-10-676-358-1

1 ETFPPKYLHYDEETSHQLLC.....QKLFLEMIGNQVQSVKISCL 380 score: Sequence: Title: Perfect :

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt 02:*

Database

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O00300 homo sanien	mus m		O08727 rattus norv			gallus	gallus		0					O6vi29 homo sapien	Aan72434 homo sapi	Q62327 mus musculu	P25119 mus musculu			P20333 homo sapien	O88734 mus musculu	Q91zm6 rattus norv	Q6vau8 rattus norv	Aaq22350 rattus no	Q80wy6 rattus norv	O98sm6 gallus gall	075509 homo sapien	Aap36088 homo sapi	Q800k7 paralichthy	
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457	655	289	289	289	467	169	278	462	276	223	277	318
14.2	14.1	13.6	13.6	13.6	13.4	12.9	12.8	12.8	12.7	12.7	12.7	12.3
297	293	284.5	284.5	284.5	279.5	270	267	267	265	264	264	257
32	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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TISSUE-Kidney,
MEDLINE-97222071; PubMed=9108485,
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Lucthy R., Mguyen H.D., Wooden S., Bennett L., Boone T., Shimmmoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Highes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

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MEDLINE-98151033; PubMed-9492069;

MEDLINE-98151033; PubMed-9492069;

MEDLINE-98151033; PubMed-9492069;

MEDLINE-98151033; PubMed-9492069;

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Sato Y., Goto M., Yamaguchi K.;

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Osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits

Osteoolastogenesis in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A., AND VARIANTS ASN-3 AND MET-104.
Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
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of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
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                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                     TILB HUMAN STANDARD, PRI, 401 AA.
000300; O60236; Q9UHP4,
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor (Osteoprotegerin) (Osteoclastogenesis inhibitory factor)
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morinaga T., Nakagawa N., Yasuda H., Tsuda B., Higashio K.; "Cloning and characterization of the gene encoding human osteoprocegerin/osteoclastogenesis-inhibitory factor."; Eur. J. Biochem. 254:685-691(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placenta;
MEDLINE=98351569; PubMed=9688283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of bone density.";
Cell 89:309-319(1997).
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
RESULT 1
T11B_HUMAN
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Richards R.D., Feingold B.A., Grouse L.H., Dorge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
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Altschul S.F., Zeeberg B. Buetow K.H., Schafer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
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Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
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Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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R. Hutterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,
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Morinaga T., Higashio K.;
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Hofbauer L.C., Neubauer A., Heufelder A.E.;
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                                                  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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MEDLINE=97312536; PubMed=9168977; DOI=10.1006/bbrc.1997.6603;
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"Isolation of a novel cytokine from human fibroblasts that
specifically inhibits osteoclastogenesis.";
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                 SEQUENCE FROM N.A., AND VARIANT ASN-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Biol. Chem. 273:5117-5123(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
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Presented the controller feator-kappaB ligand and categories and present and animative the maintaint bare diseases.", Canner 2:160-47016011.

M. Milly T. UP ARP-182 DEL. Chicaga E., King A., Wallace R., Willey J., Chicaga E., Seidel-47016011.

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M. Milly T., Seidel D., Tawkner M., Bannyld T., Callon K.E., Grey A.B., Ref I.E., Wallachen-Harder C.A., Comith J.: A ministry of the preparation of the gene Three Presents and present against the control of the gene Three Presents and the present and the present and the present and present approaches the present of th
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InterPro; IPR0100488; Death.
InterPro; IPR011029; DEATH like.
InterPro; IPR01308; TNFR_G6.
FEan; PF00020; TNFR_G6, 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR, 4.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS500505; TNFR MGFR 1; 1.
PROSITE; PS500505; TNFR MGFR 1; 1.
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02-WAR-2004 (TrEMBLrel. 27, Last ann
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                                                                                                                   EMBL; BC049782; AAH49782.1;
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                                           SEQUENCE FROM N.A.
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RX Strausberg Factor No. 1.

RX Strausberg Factor No. 1.

RX Strausberg R.L., Febigold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Atapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahay J., Helton E., Ketteman M., Madan A., Youfigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Nones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Jones S.J., Marra M.A.;

RA Machana A., Marital analysis of more than 15,000 full-length human
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                                                                                                                                                                                                     YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIBFCLKHRSCPPGFGVVQAGTPERNTV 120
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                                                                                                                                                                                                                             82 YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNIV 141
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                    Score 2079; DB 1;
Pred. No. 8.5e-140;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 QKLFLEMIGNQVQSVKISCL 380
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                                                  99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Pfam; PF00020; INFR C6; 3.
SMART; SM00005; DEATH; 1.
                                                                        Best Local Similarity 99.7
Matches 379, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Osteoprotegerin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheri
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Tnfrsf11b;
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05-JUL-2004
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                                                      Query Match
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YCSPVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTV 120
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GO; GO:0042499; P:negative regulation of odontogenesis (sensu. . ; IDA.
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                           Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.0%; Score 1834; DB 2;
Best Local Similarity 86.6%; Pred. No. 2.3e-122;
Matches 329; Conservative 25; Mismatches 26;
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NCBI_TaxID=10116;
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      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,
A blatchenko L., Marusina K., Farmer A.A., Fubin G.M., Hong L.,
Batchenko L., Marusina K., Farmer A.A., Fubin G.M., Hong L.,
Brapleton M. J. Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Branschin M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Iu K., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
A Richard W. M. Touchman J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
T. "Generation and initial analysis of more than 15,000 full-length human
T. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Rattus.
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28-FBE-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.0%; Score 1834; DB 2; Length 401; 86.6%; Pred. No. 2.3e-122; cive 25; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC049782; AAH49782.1; -.
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Name=Thfrsf11b; Synonyms=Opg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 86.6
Matches 329; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Limb;
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008727;
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                                                                                                                                                                                                                                                                                                                          Involved in dimerization (By similarity).
             TISSUB=Embryonic intestine;
MEDLINE=97262071; PubMed=9108485;
MEDLINE=97262071; PubMed=9108485;
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
Suggs S., Boyle W.J.;
"Osteopricegenin; a novel secreted protein involved in the regulation
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N-linked (Glounc. .) (Potential).
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RGD; 619802; Infrefilb.

RDD; 619802; Infrefilb.

RDD; 6198029; Infrefilb.

InterPro; IPR001029; DEATH like.

InterPro; IPR001029; DEATH like.

InterPro; IPR001020; INFR_G6;

Fam; PP00020; TNFR_C6;

SWART; SM00209; TNFR; 4.

SWART; SM00209; TNFR; 1.

PROSITE; PS50017; DEATH DOMAIN; FALSE_NEG.

PROSITE; PS50017; DEATH DOMAIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity.
Tumor necrosis factor r
superfamily member 11B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- INDUCTION: Up-regulated by osteopontin.
-!- SIMILARITY: Contains 2 death domains.
-!- SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNFR-Cys 2.
TNFR-Cys 3.
TNFR-Cys 4.
Death 1.
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1244
1455
1666
165
178
178
178
401 AA;
SEQUENCE FROM N.A.
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MEDLINE-97262071; PubMed-9108485;

MEDLINE-97262071; PubMed-9108485;

Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,

Luchty R., Mguyen H.Q., Wooden S., Bennett L., Boone T., Shimmanoto G.,

Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,

Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,

Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
                                                                                           YCSPVCKELQIVKQBCNRTHNRVCECEEGRYLELEFCLKHRSCPPGLGVLQAGTPERNTV
                                                                                                                                                                                                                        181 CEEAFFREAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKHQN
                                                                                                                                                                                                                                                                                                                                     241 KAQDIVKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP
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                                                                                                                                                                                                                                                                                                                                                                                                      301 SDQILKLISLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suggs S., Boyle W.J.; "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis."; Gene 215:339-343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILB MOUSE STANDARD; PRT; 401 AA.
008712; 070202;
28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 11B precursor (Osteoptotegerin) (Osteoclastogenesis inhibitory factor).
                                         ;
0
        Length 401;
                                       28; Indels
   87.7%; Score 1828; DB 1;
86.3%; Pred. No. 6.2e-122;
iive 24; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast; MEDLINE=98382527; PubMed=9714833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Tnfrsfilb; Synonyms=OPG, ÖCIF;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 OKLFLEMIGNOVOSVKISCL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 OKLFLEMIGNOVQSVKISCL 380
Query Match
Best Local Similarity 86.3%
Matches 328; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                         resembling osteoclastogeness.";
J. Exp. Med. 192:463-474(2000).
-! FUNCTION: Acts as a decoy receptor for RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local RANKL/OPG ratio. May also play a role in preventing arterial calcification. May act as decoy receptor for TRAIL and protect against apoptosis. TRAIL binding chocks the inhibition of osteoclastogenesis.
-! SUBCNIT: Homodimer.
-! SUBCELLULAR LOCATION: Secreted.
-! TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach, intestines and calvaria. Highly expressed in decidua and placenta, intestines.
                                                                                                                                                                                                                                                       "Osteoprotegerin reverses osteoporosis by inhibiting endosteal osteoclasts and prevents vascular calcification by blocking a process resembling osteoclastogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Involved in dimerization (By similarity).
MEDLINE=21060987; PubMed=10952716;
Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully
Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
Simonet W.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AB013998, BAA28269.1; -.
EMBL, AB013903, BAA3388.1; -.
EMBL, AB013903, BAA3388.1; -.
EMBL, AB013900, BAA3388.1; -.
EMBL, AB013900, BAA3388.1; JOINED.
EMBL, AB013901, BAA3388.1; JOINED.
EMBL, AB013902, BAA3388.1; JOINED.
HSSP, O41763; 1D0G.
HSSP, O41763; 1D0G.
GO, GO:0005578; C:extracellular matrix; IDA.
InterPro; IPR011029; DEATH like.
InterPro; IPR011029; DEATH like.
InterPro; IPR011039; Grow fac_recept.
InterPro; IPR001368; INFR_C6.
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By similarity.
By similarity.
By similarity.
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PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 2.
APODFOSIS; Glycoprotein; Polymorphi SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U94331; AAB53708.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00020; INFR c6; 3. SMART; SM00005; DEATH; 1. SMART; SM00208; INFR; 4.
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marushia K., Farmer A.R., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
N. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
N. Halton B.K., Kerteman M., Madan A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Garimwood J., Schmutz J., Nyers R.M., Butterfield Y.S.,
Arrywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
M. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILKLISLWRIKNGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLYQKL 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 CPDGFFSNETSSKAPCRKHTNCSVFGLLLIQKGNATHDNICSGNSESTQKCGIDVTLCEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCS
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                                                                                                                                                                                                                                                                                                                                                               Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein S., Strausberg R.; Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. InterPro; IPRO06209; BGF like.
InterPro; IPRO01368; TNFR c6.
Fram; PRO01209; TNFR, 4.
SWART; SM00209; TNFR, 4.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR (JFR NGFR 1; UNKNOWN 1.
PROSITE; PS00650; TNFR (JFR NGFR 2; 2.
Hypothetical protein.
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                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Dev. Dyn. 225:384-391(2002)
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                                                                                                                                                                                                                                                                           mouse cDNA sequences.
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387 AA; 4
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Best Local Similarity
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S -> A (in strain 129/0la and strain NIH Swiss).

L -> R (in strain 129/0la and strain NIH Swiss).
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                                                                                                                                                     u (GLCNAC. . .) (FOLENCIAL).
(in strain 129/Ola and strain NIH
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Nappothetical protein.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea; Pipidae;
                                                                                                                                                               By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC. ..) (Potential).
N-linked (GlCNAC. ..) (Potential).
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0
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86.1%; Pred. No. 2.3e-121;
ive 25; Mismatches 28; Indels
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N-linked
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327; Conservative
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1165
1178
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                                                                                                                                                                                                                                                                                                                                401 AA;
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                              osteoprotegerin.";
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tes 75; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22760275; PubMed=12878204;
Bridgham J.T., Johnson A.L.;
"Characterization of chicken INFR superfamily decoy receptors, DCR3
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MEDLINE=22760275; PubMed=12878204;
Bridgham J.T., Johnson A.L.;
"Characterization of chicken INFR superfamily decoy receptors, DcR3
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Biochem. Biophys. Res. Commun. 307:956-961(2003).
Biochem. Biophys. Res. Commun. 307:956-961(2003).
GOS.0004872; Fireceptor activity; IBA.
InterPro; IPR006209; BGF_like.
InterPro; IPR009109; Grow_fac_recept.
InterPro; IPR001018; Firecept.
InterPro; IPR001018; Firecept.
InterPro; IPR00118; Grow_fac_recept.
InterPro; IPR00118; Grow_fac_recept.
InterPro; IPR0118; Grow_fac_recept.
INTERPROSITE; PS01116; FGF 2; UNKNOWN 1.
IPROSITE; PS01116; INTERPROSITE; INTERPROSITE; PS00101; INTERPROSITE; PS00101; INTERPROSITE; INTERPROSIT
                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                146 AA.
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   371 LLEIFGSQTQPAKV 384
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01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
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Name≈DcR3;
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64 PVCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 PPKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 PPTYQMRDAGIKERVICQQCPFGIFVAQHCIKERPIVCAPCPDLHYTHYWNXLEKCLYCN 91
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DcR3) (M68)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
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MEDLINE=20122600; PubMed=10655513;
Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-99253915; PubMed=10318773;
MEDLINE-99253915; PubMed=10318773;
MEDLINE-99253915; Ni J., Zhai Y., Ebner R., Kwon B.S.;
"A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
J. Biol. Chem. 274:13733-13736 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.6%; Score 450; DB 2; Length 186;
48.7%; Pred. No. 3e-24;
tive 24; Mismatches 55; Indels
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Biochem. Biophys. Res. Commun. 307:956-961 (2003). EMBL; AY251406; AAP03889.1; -. GO, GO:0004872; Frsceptor activity; IEA. InterPro; IPR009030; EGF like. InterPro; IPR009030; Grow fac_recept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 CPDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 AA
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                                                                                                                                                                                       PROMITE: PSOUGES; TNER C6; 2.
SMART; SM00208; TNER; 4.
PROSITE; PSO1186; EGF 2; UNKNOWN 1.
PROSITE; PSO0652; TNER NGFR 1; 1.
PROSITE; PSS0060; TNER NGFR 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNQ186/PRO212).
Name=TNFRSF6B; Synonyms=DCR3, TR6;
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TISSUE=Fetal lung;
MEDLINE=99087326; PubMed=9872321;
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The independent of weal-ports in hamm destroint estimal tract tumors requested to the second of the independent of second of the independent of the second of the independent of the independent of second of the independent of the independent
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use: by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 LCGEREEBRACHATHURACRCRIGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-i- FUNCTION: Decoy receptor for the cytotoxic ligands TNFS14/LIGHT and TNFSF6/PASL. Protects against apoptosis.

-i- SUBCELLULAR LOCATION: Secreted.

-i- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.

Detected in adult stomach, spinal cord, lymph node, trachea, spleen, colon and lung. Highly expressed in several primary tumors from colon, stomach, rectum, esophagus and in SW480 colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKYLHYDERTSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP
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F90AEE33718449AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.1%; Score 440.5; DB 1; Length 300; 41.2%; Pred. No. 2.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor necrosis factor receptor superfamily member 6B.
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TWRR-Cys 3.

TWRR-Cys 4.

By similarity.
                                                                                                                                 SIMILARITY: Contains 4 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0006916; P:anti-apoptosis; TAS.
InterPro; IPR00930; Grow fac_recept.
InterPro; IPR001368; TNFR_GO.
Pfam; PF00020; TNFR G6; 4.
PROSITE; PS00625; TNFR NGFR 1; 1.
PROSITE; PS00625; TNFR NGFR 1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-Cys 1
                                                                                                                                                                                                                                                                       EMBL; AF104419; AAD03056.1; --
EMBL; AF134240; AAD2568.1; --
EMBL; AF217793; AAF33685.1; --
EMBL; AF217794; AAF33686.1; --
EMBL; AY358779; AAF33686.1; --
EMBL; AY31845; CAC03668.1; --
EMBL; BC017065; AAH17065.1; --
EMBL; BC017065; AAH34349.1; --
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Best Local Similarity 41...
Rest Local 77; Conservative
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EAFFRFAVPTKFTP 196
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Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-DEC-2001
01-MAR-2004
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          181
                                   71 YVKQECNRTHNRVCECKEGRYL--EIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGF 128
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PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTLC
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Bobe J., Goetz F.W.;
"A tumor necrosis factor decoy receptor homologue is up-regulated in
the brook trout (Salvelinus fontinalis) ovary at the completion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Salvelinus.
NCBI_TaxID=8038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.7%; Score 411.5; DB 2; Best Local Similarity 32.0%; Pred. No. 2.9e-21; Matches 96; Conservative 57; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salvelinus fontinalis (Brook trout) (Brook char)
                                                                                                                                                                                                                                                                                                                                                                                  302 AA
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EMBL, AF156738; AAD56428.1; -.

HSSP, O14763; 1D4V.

GO; GO:0004872; F:receptor activity; IEA.

InterPro; IPR001209; EGF like.

InterPro; IPR001209; TNFR of 4.

SMART; SMO0208; TNFR; 4.

PROSITE; PS01186; EGF 2; 1.

PROSITE; PS001205; TNFR of 4.

PROSITE; PS00523; TNFR INFR INFROMM.1.
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01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                   EEAFFRF 188
                                                                                                                                                                                                       218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Decoy TNF receptor
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SEQUENCE
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Q90W71
ID Q90W7
AC Q90W7
DT 01-DE
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124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 PVGFFSAVSSSRKACQKFSVCPPGG--TTIPGNDMNDVYCSACTNGSRTHE---GEAICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 PTYIWRDDATGDSLTCDLCAPGTYLLKHCTKDRKSDCGPCPKSHYTEIWNYIERCQYCNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PKYLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP
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"Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine with a fractalkine-like stalk and a TNF decoy receptor using cDNA fragments containing AU-rich elements.";
Cytokine 17:71-81(2002).

EMBL; AF401631; AAK91758.1; -.
HSSP; O14763; 1D0G.

GO: GO:0004872; F:receptor activity; IEA.
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Putative decoy receptor 3 protein.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNF decoy receptor.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostel; Euteleostel; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                      Pleguezuelos O., Secombes C.J., Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 AA; 31642 MW; FB75CFFC1E391AD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.2%; Score 380.5; DB 2; 38.1%; Pred. No. 4.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
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BOSP, OL763; 1D0G.

GOS.0004872; F:receptor activity; IEA.

InterPro; IPR006209; EGF_like.

InterPro; IPR009309; Grow_fac_recept.

InterPro; IPR003093; TNPR_C6.

PFam, PF00020; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00020; TNPR c6; 3.
SMART; SM02208; TNFR; 3.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNFR NGFR 2; 1.
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LOC407674
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                                                                                                                            NON TER
SEQUENCE
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Best Local
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AAH67712
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REDLINE=22388257; PubMed=12477932;

Retausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Rotatchenko L., Marusina K., Farmer A.A., Rubin G.M., Bong L.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,

Raha S.S., Couchman J.W., Green E.D., Dickson M.C., Sanchez A.,

Richards A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rodersation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                         3,
                                                                                                                                                                                                                                                                                       89 PCTADEIESVPCTQLHNRQCECKDGFYMTHGSCSRHRRCPPGEGVISNGTAHTDVKCEPC 148
                                                                                                                                                                                                                                                                                                                     PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSG--NSESTQKCGIDVTLCE 182
                                                                                                                                                                                                                                                                                                                                                  203
                                                                                                                                                                                                                                                            65 VCKELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRC 124
                                                                                                                                                                                                                                88
                                                                                                                                                                                                                       5 PKYLHYDBETSHQLLCDXCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSP
                                                                                                                                                                           Gaps
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
                                                                                                                                                DB 2; Length 285;
                                                                                                                                                                           Indels
                                                                                                                  285 AA; 31795 MW; SE3BD1B6EFC6BABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                            1.6e-18;
hes 89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOC407674 protein (Fragment).

Mann=LOC407674;

Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                             17.9%; Score 372.5;
37.6%; Pred. No. 1.6e
:ive 25; Mismatches
 InterPro; IPR009030; Grow fac_recept.
InterPro; IPR001368; TNFR_G6.
Pfam; PF00020; TNFR G6; 3.
SMART; SM00208; TNFR, 3.
PROSTTE; PS01186; EGF 2; UNKNOWN 1.
PROSTTE; PS00652; TNFR NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                183 EAFFRFAVPTKFTP 196
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                                                                                                                                                             Local Similarity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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NCBI_TaxID=7955;
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                                                                                                          Receptor.
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                                                                                                                      SEQUENCE
                                                                                                                                                   Query Match
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QGNW61
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Strausberg R.;

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A REDLINE=22380257; PubMed=12477932;

A REDLINE=22380257; PubMed=12477932;

A Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

Strausberg R.L., Feligold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Alteschul S.F., Zeeberg B., Buetow K.H., Rang J., Hsieh F.,

By Alteschul S.F., Bonaldo M.F., Carainci D., Frange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Worken N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.H., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Richards M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Reneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 KELQYVKQECNRTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVQAGTPERNTVCKRCPD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IRRLKK-----PLKQLHKRTAMRRADP 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 RFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSQEQTFQLLKLWKH-QNKAQDI
                                                                                                                                                                                                                                                                                                                                                                                  7 YLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC
                                                                                                                                                                                                                                                                                                                                                                                                             18 YRRKDPETGRILBCARCAPGSRIRQHCSSSRQTBCSPCGPGMXTEFWNYIPDCHLCDS-C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                    Length 286;
                                                                                                                                                                                                                                                                                  17.5%; Score 365; DB 2; Length 28
32.4%; Pred. No. 5.5e-18;
ive 41; Mismatches 119; Indels
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          32275 MW; 9F43CDC5FAC4E77B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-WAY-2004 (TrEMBLrel. 27, Created)
24-WAY-2004 (TrEMBLrel. 27, Last sequence update)
24-WAY-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                         Interpro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR; c6; 4.
PRART; SM00208; TNFR; c7.
PROSITE; PS01186; BGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR_NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNFR_NGFR 2; 1.
                      EMBL, BC067712; AAH67712.1; -. InterPro; IPR006209; EGF_like. InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 ALQVQQKIDIHRLEQMV-
                                                                                                                                                                                                                                                                                                                                            89; Conservative
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                                                                                                                                                                                                                                               286 AA;
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                                                                                                                                                                                                                                                                                                                   Similarity
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9
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                                                                                                                                                                                                                                                                                                                                                                    77 ABHQRVVQPCNGIANTVCECEEGFYWEQHFCRRHSVCRPGHGVKTAGTPYSDTVCEACAE 136
                                                                                                                                                                                                                                                                                                                                                                                                               127 GFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTLCEEAFF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187 RFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRCHSSQEGTFQLLKLWKH-QNKAQDI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---PLKQLHKRTAMRRADP 234
                                                                                                                                                                                                                                                                                          18 YRRKDPETGRILECARCAPGSRLRQHCSSSRQTECSPCGPGMYTEFWNYIPDCLLCDS-C 76
                                                                                                                                                                                                                                                                   7 YLHYDEETSHQLLCDKCPPGTYLKQHCTAKWKTVCAPCPDHYYTDSWHTSDECLYCSPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
PubMed=14688072;
Lainez B., Fernandez-Real J.M., Romero X., Esplugues E., Canete J.D.,
Ricart W., Engel P.;
                                                                                                                                                                                                                                     26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and characterization of a novel spliced variant that encodes human soluble tumor necrosis factor receptor 2."; Int. Immunol. 16:169-177(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble tumor necrosis factor receptor superfamily member 1B.
Homo sapiens (Human).
                                                                                                                                                                                            Query Match 17.5%; Score 365; DB 2; Length 286; Best Local Similarity 32.4%; Pred. No. 5.5e-18; Matches 89; Conservative 41; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.2%; Score 337; DB 2; Length 26:
40.4%; Pred. No. 5e-16;
tive 16; Mismatches 71; Indels
                                                                                     Strausberg \bar{R} ; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                           286 AA; 32275 MW; 9F43CDC5FAC4E77B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 AA; 28481 MW; D29A489610A4354A CRC64;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 ALQVQQKIDIHRLEQMV-----IRKLKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 VKKIIQDIDLCENSVQRHIGHANLTFEQLRSLMES 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 SEGLIDRSMALENSYLSHI.--AQRMTQNIRRVQQS 267
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GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR011368; TNFR.cc.
Pfam; PF00020; TNPR.cf.
PIRSF; PIRSF01968; TNFR. 2; 1.
PROSITE; PS00052; TNFR, 4.
PROSITE; PS00052; TNFR, 4.
PROSITE; PS00052; TNFR, 4.
PROSITE; PS00050; TNFR, 4.
                                                                                                                       EMBL; BC067712; AAH67712.1;
NON TER 1 1 1 SEQUENCE 286 AA; 32275 MW
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Best Local Similarity 40.4%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                    SEQUENCE FROM N.A
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                                                                        TISSUE=Embryo;
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12; Gaps

Length 268;

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69 LOYVKQECNRTHNRVCECKEGRYLEI-----EFCLKHRSCPPGFGVVQAGTPERNTVCK 122
163 PCAPGTFSNTTSTDICRPHQICNVVAI----PGNASMDAVCTSTS 204
                                                                                   123 RCPDGFFSNETSSKAPCRKHINCSVFGLLLIQKGNATHDNICSGNS 168
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